```
SEQUENCE FROM N.A.

STRAIN=FVB/N; TISSUE=Liver;

AX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

RA Aleschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninoi P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninoi P., Wallach F.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Roback S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley D.M., Sodreja A.N., Gayb L.J., Hulyk S.W.,

RA Richards S., Worley D.M., Sodreja A.N., Gabb R.A.,

RA Villalon D.K., Marny D.M., Sodreja A.N., Gabb R.A.,

RA Richards S., Worley A.C., Shevchenko Y., Bouffard G.G.,

RA Richards A.C., Grimwood J., Schmutz J., Myers R.M.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Blakesley R.W., Touchman J.W., Green E.D., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length

Puman and mouse cDNA sequences.",

Purcham and mouse cDNA sequences.",
180
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                                                                                                                                                                  SERRSDWAHHPTFRKIYCDAVPYLFKKVRAVYTEGGWFEEGWKLEAIDPLNLGNICVATV 240
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                                                                                                   CKVILLDGYLMICVDGGPSTDGLDWFCYHASSHAIFPATFCQKNDIELTPPKGYEAQTFNW
                                                                                                                                                                                                                                                                                       CKVLLDGYLMICVDGGPSTDGLDWFCYHASSHAIFPATFCQKNDIELTPPKGYEAQTFNW
                                                                     VVDKSQVSRTRMAVVDTVIGGRLRLLYEDGDSDDDFWCHMWSPLIHPVGWSRRVGHGIKM
                                                                                                                                                                                                       391 SERRSDMAHHPTFRKIYCDAVPYLFKKVRAVYTEGGWFEEGWKLEAIDPLNLGNICVATV
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28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Lethal(3)malignant brain tumor-like 2 protein (L(3)mbt-like 2 protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DGWDSEYDQWYDCESPDIYPVGWCELTGYQLQPPVAAEPATPLKAKBATKKKKKQFGKKR
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Mammalia; Eutheria; Rodentia; Sciurognathi, Muridae; Musinae; Mus
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P59178;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMEL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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complex suggests that it may contribute to prevent expression of genes that trigger the cell into mitcsis (By similarity).

-!-SUBURIT: Part of the E2F6.com-1 complex in G0 phase composed of E2F6, MGA, MAX, TFDP1, EAR3, BAT8, EUHMTASE1, RING1, RNF2, MBLR, BAT8 and YAP2 (By similarity).

-!-SUBCENLUAR LOCATION: Nuclear (Probable).

-!-SUBCENLUARITY: Contains 1 C4-type zinc finger.

-!-SIMILARITY: Contains 4 MBT domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            211 MKGMKVBVLNSDAVLPSRVYWIATVIQAAGYRVLLRYBGFENDASHDFWCNLGTVDVHPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SDRRCDMSHHPTFRKIYCDAVPYLFKKVRAVYTEGGWFEEGMKLEAIDPINIGSICVATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CKVLLDGYLMICVDGGPSTDGSDWFCYHASSHAIFPATFCQKNDIELTPPKGYETQPFAW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SERRSDMAHHPTFRKIYCDAVPYLFKKVRAVYTEGGWFEEGMKLEAIDPLNLGNICVATV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               331 VVDKTQVSRTRMAVVDTVIGGRLRLLYEDGDSDDDFWCHMWSPLIHPVGWSRRVGHGIKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CKVLLDGYLMICVDGGPSTDGLDWFCYHASSHAIFPATFCQKNDIBLTPPKGYBAQTFNW
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                                                                                                                                                                                                                                                                                                                                    Transcription: Transcription; Chromatin regulator; Nuclear protein; Zinc-finger; Metal-binding; Repeat.
ZN FING 90 114 C4-TYPE.
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89.7%; Pred. No. 1.6e-195;
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MBT 3.
MBT 4.
POLY-GLU.
POLY-LYS.
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MGD, MGI:2443584, 4732493N06Rik.
SMART; SW00561, MHT; 4
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17
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703 AA;
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/codon_start=1
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/product="H-1(3) mbt-like protein"
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TGQLADGTPTGQDALVLGFDWGKFLKDHSYKAAPVSCFRHYDLYDOWEDVWKGMKVEV
LNSDAVLDSRYYMANSVIGTGRYLLKPGFENDASHDFWCLLGTTVDVHPIGWCAIN
SKILVPPRTTHAKFTDWKGYTMKRLVGSRTLPVDFHIKWYESKKYPPRGGMRLEVVDK
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SKLILVPBATTHAKFTDWKGYTMKRLYGSRTLYPGGWREEGWLLBATDFHLGATTV
CKVLLDGYLAICVDGGPSTDGLDWRCYHASSHAIPPRTFCGKNDIELTPPKGYFEAGTF
CKVLLDGYLAICVDGGPSTDGLDWRCYHASSHAIPPRTFCGKNDIELTPPKGYFEAGTF
NWENYLEKTKSKAAPSRLFNWDCPNHGFKVGMKLEAVDLMSPRLICUYATVKRVURELL
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QFGKKRKRIPPTKTRPLRQGSKKPLLEDDPQGARKISSEPVPGEIIAVRVKEEHLDVA
SPDKASSPELPVSVENIKQETDD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 AACGGCTGGGGCTCCAGGACGCTTCCCGTGGATTTCCACATCAAGATGGTGGAGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 935 AACGGCTGGTGGGCTCCAGGACGCTTCCCGTGGATTTCCACATCAAGATGGTGGAGAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 TGAAGTACCCCTTTAGGCAGGCATGCGGCTGGAAGTGGTGGACAAGTCGCAGGTGTCAC
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                                                                                  /note="alternative variant a"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.9%; Score 2553.4;
100.0%; Pred. No. 0;
ive 0; Mismatches
                  /gene="H-1(3)mbt-like<sup>r</sup>
                                    40. .2157
/gene="H-1(3)mbt-like
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Matches 2554; Conservative
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Homo sapiens mRNA for H-l(3)mbt-like protein, alternative variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2281 GAAGCCCCCTAAAAAAAATCATCCAAGATTCCTTTGTAGTTAAAGGGTCCAGTTCTGA 2340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGAAACCATGCCTGGAGGGCCGTGAACACAGAACCCTCAAGACAAAGGATGACAGAGCT 2460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ., Johannes Gutenberg Universitaet, 32, 55099 Mainz, GERMANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AJ305226.1 GI:13940238
alternative splicing; H-1(3)mbt-like gene; H-1(3)mbt-like protein.
Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                         2041 CTCAGCCTCATGTGTTGGTCCTCTGCTCCTCCTAGCTCCCCAGGGAATGTTGGGGAACCCAG
                                      GACAGTGAGTTGTGTGGTGGGGGGCAGCCTCTGCCTCAAAAATTCACCAAAAATGCCT
                                                                                                                                                                                    CTTGTCTCGGCAGCTAAGAAGCAGTGACCAGGATGTGGATTTTTGGCGACCTGTGTGGTGG
                                                                                                                                                                                                                    CTTGTCTCGGCAGCTAAGAAGCAGTGACCAGGATGTGGGATTTTTGGCGACCTGTGTGGTGG
                                                                                                                                                                                                                                                                              CCTTGAGCTGCTTTCTGTGTTTGTGAGGACTGACTCCCATTTCCTAAAGGAAATGCCCCC
                                                                                                                                                                                                                                                                                                                                                                                                       2221 GGGGAGGACATIGGGGAGGAAGATGGCCTGAGTGTGCACTTTGGCTCTGCTACCTGCTCCT
                GACAGTGAGTTGTGTGGGGGGGGCGCCTCTGCCTCAAAAATTCACCAAGAAATGCCT
                                                                                                                                                                                                                                                                                                       2161 CCTTGAGCTGCTTTCTGTGTTTTGTGAGGACTGCCCATTTCCTAAAGGAAATGCCCCC
                                                                                                                                                                                                                                                                                                                                                           GGGGAGGACATTGGGAGGAAGATGGCCTGAGTGTGCACTTTGGCTCTGCTACCTGCTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAGCCCCGCTAAAAATAATTCATCCAAGATTCCTTTGTAGTTAAAGGGTCCAGTTCTGA
                                                                                                  CTCAGCCTCATGTTGGTCCTCTGCTCCTCCTAGCTCCCCAGGGATGTTGGGGACCCAG
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Submitted (15-JAV-2001) Wismar J.,
Institut fuer Genetik, Becherweg 32
Location/Qualifiers
1, 3194
/ Organism="Homo sapiens"
/ mol_type="mRNA"
/ db_xref="taxon:9606"
/ db_xref="taxon:9606"
/ db_raf="12"
/ map="12"
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FEBS Lett. 507 (1), 119-121 (2001)
21538645
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HSA305226
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
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PUBMED
REFERENCE
AUTHORS
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211 MKGMKVEVLNSDAVLPSRVYWIASVIQTAGYRVLLRYEGFENDASHDFWCNLGTVDVHPI 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- CAUTION: Ref.3 sequences differ from that shown in that they seem to include intronic sequence.-!- CAUTION: Ref.4 sequence differs from that shown due to erroneous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
100.0%; Score 2683; DB 1; Length 705;
Best Local Similarity 100.0%; Pred. No. 3.8e-216;
Matches 495; Conservative 0; Mismatches 0; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Missing (In 1soferm 2).
/FTId=VSP 003905.
EPATPLKAXE -> GVGSRGPKRL (in 1soform 3).
complex suggests that it may contribute to prevent expression of genes that trigger the cell into mitosis.
                           SUBUNIT: Part of the E2F6.com-1 complex in G0 phase composed of E2F6, MGA, MAX, TFDP1, CEX3, BAT8, EUHMTASE1, RING1, RNF2, MBLR, MAX, TABP1, CEX3, BAT8, EUHMTASE1, RING1, RNF2, MBLR, MBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transcription regulation; Chromatin regulator; Nuclear protein;
Zinc-finger; Metal-binding; Repeat; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPATPLK -> GKLPRSL (in isoform 2) /FTId=VSP_003904.
                                                                                                                                                                                                                                                                             Name=2; Synonyms=B;
IsoId=Q969R5-2; Sequence=VSP_003904, VSP_003905;
                                                                                                                                                                                                                                                                                                                                                               IsoId=0969R5-3; Sequence=VSP_003906, VSP_003907;
-!- SIMILARITY: Contains 1 C4-type_zinc finger.
-!- SIMILARITY: Contains 4 MBT domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /FTId=vSP_003906.
Missing (In isoform 3).
/FTId=vSP_003907.
R -> W (IN dbSNP:2277846)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FTId=VAR 015093,
8FC86A440982FFA7 CRC64;
                                                                                                                                                                                           Event=Alternative splicing; Named isoforms=3;
                                                                                                                                     -!- SUBCELLULAR LOCATION: Nuclear (Probable).
                                                                                                                                                                                                                                                     IsoId=Q969R5-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, AJ305226; CAC37794.1; -.
EMBL, AJ30527; CAC37795.1; -.
EMBL, AL136564; CAB66499.1; -.
EMBL, AKO74091; BAB84917.1; ALT_SEQ.
EMBL, AKO77052; BAC04936.1; ALT_SEQ.
EMBL, AL035681; -; NOT_ANNOTATED_CDS.
EMBL, AL035681; CAB63071.1; ALT_SEQ.
EMBL, BC017191; AAH17191.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene model prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GK; Q969RS; -. InterPro; IPR004092; Mbt. Pfam; PF02820; mbt; 4. SMART; SMO561; MBT; 4.
                                                                                                                                                                                                                             Name=1; Synonyms=A;
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DOMAIN 21
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61 GWCAINSŘÍLVPPRTIHAKFIDWKGYLMKRLVGSRTLPVDFHIKMVESMKYPFRQGMRLE 120

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/ Fri Feb

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

February 4, 2004, 09:05:51; Search time 18 Seconds (without alignments) 1293.234 Million cell updates/sec Run on:

US-10-031-915-36 2683 1 MKGMKVEVLANSDAVLPSRVY......KASSPELPVSVENIKQETDD 495 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 segs, 47026705 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_41:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SIDMMARIES

	Description	Q969rs homo sapien	mus m	Q9y468 homo sapien	P98167 bos taurus	mycor	рошо	рошо	bos t		homo sap	torpedo	candi	P58397 homo sapien		sacch		caenc							rattı		rattı	P05892 simian immu		P36002 saccharomyc	0	9	-	Q9y8h5 mortierella
SUMMARIES	ID	LML2 HUMAN	LML2 MOUSE	LMBT HUMAN	SSPO_BOVIN	RL29_MYCGE			PAP BOVIN	PAP MOUSE	Z198_HUMAN		CBF5_CANAL	AT12_HUMAN	H1 MAIZE	EAF3_YEAST	HS1_HUMAN	SDC3 CAEEL	GAG_SIVA1	NEH HUMAN	CPSQ_CANMA	ANK2_HUMAN	NRP2_MOUSE	HILYCPN	MAPB RAT	SMA3 HUMAN	NRP2 RAT	GAG_SIVAT	VP53 BPAPS	PTK1 YEAST	CORO_YEAST	SYEP_DROME	ABC2_MOUSE	FD12_MORAP
	ength DB	705 1	703 1		867 1	•	• •	• •	738 1	• •	٠.	•	•	1593 1		401 1	486 1	2150 1	520 1							н	-	Н	Н	Н		1714 1	434	
•	* Query Match Length	100.0	90	g	4.5	4.3	4.1	3.9	3.7	3.7	3.6	3.6	3.4	3.4	3.4		3.4	3.4											3.2			3.2	٠	•
	Score	2683	2436	510	121	$\overline{}$	109.5	104	98.5	98.5	96.5	95.5	ä	92.5	Ή.	91	91	90.5	90	90	89.5	89	88.5	88	88	87.5	۲.	87	ġ.	ġ.	ė.	86.5	Ġ	98
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Q09178 cyprinus ca O93794 candida gla	P07814 homo sapien P04335 escherichia			P57254 buchnera ap Q8ztz0 p glucosami	P29190 haemonchus	рошо	P46821 homo sapien
JAK1 CYPCA TOP1 CANGA	SYEP_HUMAN YAFA_ECOLI	SYA THEVO FD12 MORIS	PAP2_XENLA	NUCD BUCAI GLMS PYRAE	PPCK_HAECO	NFC3_HUMAN	MAPB_HUMAN
			н.		٦	Н	-
1156 1406	1440	876 400	484	600 601	619	1075	2468
е и 2 2	а в 7	3.5	3.2	w w 0 0	3.2	3.5	3.2
86 86	86 85.5	85.5 85	80	8 8 8 2	85	82	89
34 35	37	8 6 6 7	40	4 4 2 7	43	44	45

## ALIGNMENTS

RESULT 1

8 & 8 &

GAAGGCTAGGCCCAGAACTCGTTAAAATTCCCCCCCAACCCACCAAGCTCAAGCCTCAAGGCCCCAAGACTCCTTAAAATTCCTTAAAATTCCCCCCCC	3095 2521 3155 3155 310N 10N 10N 10N 10N 10N 10N 10N 10N 10N
ATTGACC 720	2074 Db 2074 Qy 1500 Db 2134 Eb 2194 DB 1620 AC 2254 AC 2254 KE 1680 SO 2314 KB

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

February 4, 2004, 09:05:51; Search time 18 Seconds (without alignments) 1293.234 Million cell updates/sec

Title: Perfect score: Sequence:

US-10-031-915-36 2683 1 MKGWKVEVLNSDAVLPSRVY.......KASSPELPVSVENIKQETDD 495

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

127863 seqs, 47026705 residues Searched:

Total number of hits satisfying chosen parameters:

127863

Minimum DB seg length: 0 Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_41:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SIMMARIES

	Description	Q969r5 homo sapien	mus m	Q9y468 homo sapien		P47405 mycoplasma		рошо	bos t	Q61183 mus musculu				P58397 homo sapien							Q12587 candida mal	Q01484 homo sapien										dro	BUM	Q9y8h5 mortierella
SUMMARIES	QI QI	LML2 HUMAN	LML2 MOUSE	LMBT HUMAN	SSPO_BOVIN	RL29 MYCGE	TAC2_HUMAN	NEBU_HUMAN	PAP_BOVIN	PAP_MOUSE	Z198 HUMAN	ENP1_TORCA	CBF5 CANAL	AT12 HUMAN	H1 MAIZE	EAF3_YEAST	HS1_HUMAN	SDC3_CAEEL	GAG SIVA1	NFH_HUMAN	CP5Q_CANMA	ANK2_HUMAN	NRP2 MOUSE	H1_LYCPN	MAPB RAT	SMA3_HUMAN	NRP2_RAT				CORO_YEAST		ام	FD12_MORAP
	ry ch Length DB	.0 705	.8	.0 772		200	1026	6999	738		1377	721	479	1593	245	401	486	2150	520	1020		3924	931	3 202	2459	425	925	519	307	260	651		2434	400
dhe	Query Score Match	2683 100	σ			•											m		m		89.5		m	m	m		m							
	Result No.	1	71	m	4	ស	ø	7	80	σ	10	11	12	13	14	15	16	17	18	13	90	21	22	23	24	25	56	27	28	53	30	31	32	33

009178 cyprinus ca 093794 candida gla P07814 homo sapien	P04335 escherichia Q97ah7 thermoplasm P59668 mortierella	P57254 buchnera ap Q8ztz0 p glucosami P29190 haemonchus	
JAKI_CYPCA TOPI_CANGA SYEP_HUMAN	YAFA_ECOLI SYA_THEVO FD12_MORIS	NUCD BUCAI GLMS PYRAE PPCK HAECO	NFC3_HUMAN MAPB_HUMAN
1156 1406 1440	414 876 400 400	600 601 619	1075 2468
6 6 6 6 6 6 6 6	w w w w		m m
8 8 8 8 6 8 6	885 55.5 85.5 85.5	00 00 00 O1 D1 D1 D1	80 80 51 57
3 3 4 3 5 5 3 5	2 8 8 8 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	1 4 4 4 5 4 6 6	4 4 5

## ALIGNMENTS

	RESULT.  IMAL2 HUMAN  ID LML2 HUMAN  ID LML2 HUMAN  C OSGSES, OBTENI, OSSGSC, OSBOLE  DT 28-FEB-2003 (Rel. 41, Created)  DT 28-FEB-2003 (Rel. 41, Created)  DT 28-FEB-2003 (Rel. 41, Created)  DT 28-FEB-2003 (Rel. 42, Last sequence update)  DT 15-SEP-2003 (Rel. 42, Last sequence update)  E Lethal(3)malignant brain tumor-like 2 protein (L(3)mbt-like 2 protein)  E Lethal(3)mbt-like protein)  C Mammalis, Butheria; Primates; Catarrhini; Hominidae; Homo.  C MAMMalis, Butheria; Primates; Catarrhini; Hominidae; Homo.  C MAMMalis, Butheria; Primates; Catarrhini; Hominidae; Homo.  C MAMMALS ENDINE-21539645; PubMed=11682070;  RY MEDLINE-21539645; PubMed=11682070;  RY MEDLINE-21539645; PubMed=11682070;  RY MEDLINE-21539645; PubMed=11230166;  RA MEDLINE-21539645;  RA MEDLINE-2153964
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RA Conroy D., Corby N.R., Ceville G.J., Cox A.V., Davis J., Dawson B., Brans P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G., Evans L., Garard M.E., Garard M.E., Garard M.R., Graffeths M.N.D., Hall C., Rall R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S., Hall R.E., Jones M.C., Kershaw D.V., Kimberley A.M., King A., Hall C., Rartyn I.D., Mashredin Mohammadi M. Matthews D.H., Mccann O.T., Mclaren S., McMurray A.A., Milne S.A., Mortimore B.J.C.T., RA Phillips S.H., Plumb R.W., Ramsay H., Ramsay Y., Rogers L., Ross M.T., Scott C.E., Schra H.K., Skuce C.D., Smalley S., Smith M.L., Steward C.A., Sulston J.E., Swann R.M., Audin M., Wallis J.M., Williamson H., Willey D.L., Milliams S.A., Williamson H., Willey D.L., Milliams S.A., Williamson H., Willey D.L., Rawashki K., Sasaki T., Asakawa S., Rudoh J., Shimizu N., Milliams S.A., Shibuya K., Yangitaki Y., Aoki N., Mitesyama S., Romen R., Shibuya K., Yangitaki Y., Aoki N., Mitesyama S., Romen R., Shibuya K., Yangitaki Y., Aoki N., Mitesyama S., Roman S., Shibuya K., Yang C., Hubard T., Bentley D.R., Backsun S., Do A., Do T., R. Dorman A., Shibuya K., Yang C., Mang Y., Hu P., Malaj E., Nguyen T., Pan H., Rawis G., Bentley D., Shaull S., Slan D., Song D., R. Amang G., Wang Y., Hu P., Malaj E., Nguyen T., Pan H., Rawis G., Bentley D., Bradshaw H., Bourne S., R. Murray J., Miller N., Minx P., Cordes M., Do T., R. Miller S., Murray J., Miller N., Minx P., Cordes M., Do S., Pallon D., Bemis G., Bentley D., Bradshaw H., Bourne S., R. Annoshim G., Chan K., Kemp K., Latraille P., Layman D., Bradshaw H., Bourne S., R. Korf I., Bedell J.A., Milliar D., Waterston R., Waterston R., Wilson R., Wilkinson P., Bodenteich A., Wang Q., Chinson A., Wong A.C.C., Morrow B.E., Edelmann L., Kards B., Shaikh T., Kurahashi H., Saitta S., Budarf M., Shaikh T., Rharman R., Hu K., Hu K., Khan A.S., Lane D., Hartman R., Hu K., Khan A.S., Lane D., Hartman R., Hu K., Hartman R., Hartman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wilkinson P., Bodenteich A., Hartman K., Hu
Tilahun Y., Wright H.;
"The DNA sequence of human chromosome 22.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 402:489-495(1999)
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DECEMBER FROM N.A. (150FORM 17).

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REDINE=22388257; PubMed=12477932;

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Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haie F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Anglek J.A., Gunaratne P.H.,

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Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahas S.Y., McZwan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rahas S.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Schmitz J., Myers R.M.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Generation and initial analysis of more than 15,000 full-length

Numan and mouse cDNA sequences. Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

EDINITIFICATION OF COMPLEX WITH E2F6; TFDP1; MAX; MGA; EUHMTASE1; CBX3; RING1; RNF2; MBLR; BATS AND YAF2.

MEDLINE=21999559; PubMed=12004135; MEDLINE=21999559; PubMed=12004135; MEDLINE=21999559; PubMed=12004135; MEDLINE=21999559; PubMed=12004135; MEDLINE=21999559; MEDLINE=21999559; MEDLINE=21999559; MEDLINE=21999559; MEDLINE=219995959; MEDLINE=219995959; MEDLINE=2199659; MEDLINE=2199659; MEDLINE=2199659; MEDLINE=2199659; MEDLINE=2199659; MEDLINE=219969; MEDLINE=2199699; MEDLINE=2199699; MEDLINE=2199699; MEDLINE=2199699; MEDLINE=2199699;

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). ö 211 MKGMKVBVLNSDAVLPSRVYWIASVIQTAGYRVLLRYBGFENDASHDFWCNLGTVDVHPI 270 GWCAINSKILVPPRTIHAKFTDWKGYLMKRLVGSRTLPVDFHIKMVESMKYPFRQGMRLE 120 9 MBT 1.
MBT 2.
MBT 2.
MBT 3.
MBT 4.
MBT 4.
MBT 4.
POLY-GLU.
POLY-LUS.
EPATPLK -> GKLPRSL (in isoform 2).
/FTIG=VSP 003905.
/FTIG=VSP 003905.
/FTIG=VSP 003905.
MISSING (in isoform 3).
/FTIG=VSP 003906.
MISSING (in isoform 3).
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/FTIG=VSP 003907.
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-!- SIMILARITY: Contains 1 C4-type\_zinc finger.
-!- SIMILARITY: Contains 4 MBT domains.
-!- CAUTION: Ref.3 sequences differ from that shown in that they seem 1 MKGMKVEVLNSDAVLPSRVYWIASVIQTAGYRVLLRYEGFENDASHDFWCNLGTVDVHPI Gaps to include intronic sequence. -!- CAUTION: Ref.4 sequence differs from that shown due to erroneous gene model prediction. complex suggests that it may contribute to prevent expression of genes that trigger the cell into mitosis. SUBUNIT: Part of the E2F6.com-1 complex in G0 phase composed of E2F6, MGA, MAX, TFDP1, CBX3, BAT8, EUHMTASE1, RING1, RNF2, MBLR, Pfam; PF02820; mbt; 4. SMART; SM00561; MBT; 4. Transcription regulation; Chromatin regulator; Nuclear protein; Zinc-finger; Metal-binding; Repeat; Alternative splicing; ., Length 705; Indels /FTId=VAR\_015093. 705 AA; 79110 MW; 8FC86A440982FFA7 CRC64; Name=2; Synonyms=B; IsoId=2969R5-2; Sequence=VSP\_003904, VSP\_003905; 100.0%; Score 2683; DB 1; ilarity 100.0%; Pred. No. 3.8e-216; Conservative 0; Mismatches 0; Event=Alternative splicing; Named isoforms=3; BATB and YAF2.
SUBCELLULAR LOCATION: Nuclear (Probable).
ALTERNATIVE PRODUCTS: Name=1; Synonyms=A; IsoId=Q969R5-1; Sequence=Displayed; EMEL, AL136564; CAB66499.1; -..
EMEL, AKO74091; BAB84917.1; ALT SEQ.
EMEL, AKO97052; BAC04936.1; ALT SEQ.
EMEL, AL03568; -; NOT ANNOTATED CDS.
EMEL, AL035681; CAB63071.1; ALT SEQ.
EMEL, BCO17191; AAH77191.1; -..
Genew, HGNC:18594; L3MBTL2. C4-TYPE. EMBL; AJ305226; CAC37794.1; -. EMBL; AJ305227; CAC37795.1; -. IPR004092; Mbt. 300 617 705 Local Similarity hes 495; Conserv 540 17 620 608 618 300 615 609 Polymorphism. GK; Q969R5; Name=3 nterPro; SEQUENCE Query Match /ARSPLIC VARSPLIC MARSPLIC MARSPLIC VARIANT DOMAIN DOMAIN Best Loca Matches + 엄 ð 8 m

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REQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=FVB/N, TISSUE=Liver;

MEDLINE=238825; PubMed=12477932;

MEDLINE=238825; PubMed=12477932;

A trausherg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A trachenko L., Marusina K., Farmer A.A., Rubin G.M., Haich F.,

A trapleton M., Soares M.B., Bonaldo M.F., Carnhori P., Frange C.,

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B cappleton M., Soares M.B., Bonaldo M.F., Carnhori P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B saks S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunzarne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glbbs R.A.,

A Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glbbs R.A.,

A Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glbbs R.A.,

A Halton M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Raha S.N., Comman J.W., Green E.D., Dickson M.C.,

B lakeeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

B utterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

R.Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences.",

P.FO. NATI A.A.

P.FUNCTION: Putative Polycomb group (PGS) protein.

P.FO. NATI A.A.

Manntain the transcriptionally repessave etate of genes, probably

via a modification of chromatin, rendering it heritably changed in
CKVLLDGYLMICVDGGPSTDGLDWPCYHASSHAIFPRAFFCQKNDIELTPPKGYZAQTFNW 510
                                                                                                             180
                                                                                                                                                            VVDKSQVSRTRMAVVDTV1GGRLRLLYEDGDSDDDFWCHMWSPLIHPVGWSRRVGHGIKM 390
                                                                                                                                                                                                                                            SERRSDMAHHPTFRKIYCDAVPYLFKKVRAVYTEGGWFEEGMKLEAIDPLNLGNICVATV 240
                                                                                                                                                                                                                                                                                                              SERRSDMAHHPTFRKIYCDAVPYLFKKVRAVYTEGGWFEEGMKLEAIDPLNLGNICVATV 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DGWDSEYDQWVDCESPDIYPVGWCELTGYQLQPPVAAEPATPLKAKEATKKKKKQFGKKR 420
                                                                                                     VVDKSQVSRTRMAVVDTVIGGRLRLLYEDGDSDDFWCHMWSPLIHPVGWSRRVGHGIKM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
Le-SEP-2003 (Rel. 42, Last annotation update)
Lechal(3)malignant brain tumor-like 2 protein (L(3)mbt-like 2 )
(H-1(3)mbt-like protein)
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FNBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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expressibility. Its association with a chromatin remodeling
                                complex suggests that it may contribute to prevent expression of genes that trigger the cell into mitosis (By similarity).
SUBUNIT: Part of the ESF6.com-1 complex in G0 phase composed of E2F6, MGA, MAX, TEDP1, CBX3, BAT8, EUHMTASE1, RING1, RNF2, MBLR, BAT8 and YAF2 (By similarity).
SUBCELLULAR LOCATION: NUCLEAR (Probable).
SIMILARITY: Contains 1 C4-type zinc finger.
SIMILARITY: Contains 4 MBT domains.
                                                                                                                                                                                                                                                                                                                                         MGD; MGI:2443584; 4732493NG6Rik.
SMART; SM00561; MBT; 4.
Transcription regulation; Chromatin regulator; Nuclear protein;
Zinc-finger; Metal-binding; Repeat.
ZN FING 214 291 MBT 1.
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89.7%; Pred. No. 1.6e-195;
ive 23; Mismatches 26;
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MBT 3.
MBT 4.
POLY-GLU.
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WEDLINE=21638749; PubMed=11780052;
WEDLINES OF P. Black G. A. Barde L.M., Beard D.M.,
WEDLINES OF P. Black G. P., Black G. Carter N.P.,
WEDLING G. C.,
WEDLING G. Carter C. Carter N.P.,
WEDLING G. C.,
WEDLING G. Carter G.,
WEDLING G. Carter N.P.,
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IShikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,
Sotani H., Nomira N., Ohara O.;
Fotani H., Nomira N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. X.
The complete sequences of 100 new cDNA clones from brain which can
code for large proteins in vitro.";
DNA Res. 5.169-176(1998).
In FUNCTION: Polycomb group (FcG) protein. PcG proteins maintain the
transcriptionally repressive state of genes, probably via a
modification of chromatin, rendering it heritably changed in its
expressibility. Probably plays a role in cell proliferation.
Overexpression induces multinucleated cells, suggesting that it is
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                O99468, O9HIES; O9HIGS; O9UGO6; O9UJB9; O9Y4C9; 28-PEB-2003 (Rel. 41, Created) 28-PEB-2003 (Rel. 41, Created) 28-PEB-2003 (Rel. 41, Last sequence update) 15-SEP-2003 (Rel. 42, Last amonation update) Lethal (3)malignant brain tumor-like protein (L(3)mbt-like) (L(3)mbt Danalto Danalto Danalto Danalto Raylos (H-1(3)mbt protein) (H-L(3)mbt Danalto Raylos (H-1(3)mbt Danalto Raylos (H-1(3)mbt Danalto 
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99373015; PubMed=10445843;
Koga H., Matsui S.-I., Hirota T., Takebayashi S.-I., Okumura K.
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Koehrer K., Beyer A., Mewes H.-W., Gassenhuber J., Wiemann S.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
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HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARIVEVITYSEGKTLYWITYAQLGDLYCSDHLOEGKGILETGY HSLLCSLPTHLLAKLSFASDSQY -> VRCKCRVGDRAGYT VLKTAGSRCPPQRHFC (in isoform 2 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARIVRVTHVSGKTLVWTVAOLGDLVCSDHLQEGKGILETGV
HSLLCSLPTHLLAKLSFASDSQY -> MIDGEAFLLLTQAD
                                                                                                                                                                                                   Isold=Q9Y468-4; Sequence=VSP 003903; ISSUE SPECIFICITY: Widely expressed. Expression is reduced in colorectal cancer cell line SW480 and promyelocytic leukemia cell
                                                                                                                                                                                                                                                                                                                           -1- SIMILARITY: Contains 3 mbt domains.
-1- CAUTION: Ref.3 (CAC18508) sequences differ from that shown due to erroneous gene model prediction.
required to accomplish normal mitosis.
SUBCELLULAR LOCATION: Nuclear; excluded from the nucleolus. Does not colocalizes with the PcG protein BMII, suggesting that these two proteins do not belong to the same complex.
ALTERNATIVE PRODUCTS:
Event_Alternative splicing; Named isoforms=4;
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IVKIMSVKLGPALKIYNAILMFKNADDTLK (in
                                                                                                                                                                                                                                                 line HL-60.
DEVELOPMENTAL STAGE: In interphase cells, it is scattered throughout the nucleoplasm. In mitotic cells, it strongly associates with condensed chromosomes from the prophase to
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/FIGL4VSR 003903.
P -> L (IN RBF. 1).
LR -> MC (IN RBF. 1).
L -> M (IN RBF. 1).
S -> P (IN RBF. 1).
H -> M (IN RBF. 1).
                                                                                                                                                        Name=3;
IsoId=Q9Y468-3; Sequence=VSP_003901, VSP_003902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Missing (in isoform 3). /FIId=VSP_003901.
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                                                                                       Name=1; Synonyme=mbt-1;
IsoId=Q9X468-1; Sequence=Displayed;
Name=2; Synonyms=mbt-11;
IsoId=Q9X468-2; Sequence=VSP_003902;
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EMBL; Z98752; CAC16800.1; -.
EMBL; Z98752; CAC18508.1; -.
EMBL; ALO31681; CAC17518.1; ALT_SEQ.
EMBL; ALO31681; CAR4359.1; -.
EMBL; AB014581; BAA31656.1; -.
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348
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321 LR
332 L
595 S
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Pfam; PF02820; mbt; 3.
Pfam; PF01530; zf-C2HC; 1.
SMART; SM00561; MBT; 3.
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GK; Q9Y468; -.
InterPro; IPR004092; Mbt.
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DNA-binding; Nuclear prote
DOMAIN 242 315
DOMAIN 349 422
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332
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772 AA;
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TESP TYPE-1 3.

TESP TYPE-1 4.

BY SIMILARITY.

BY SIMILARITY.
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20.8%; Pred. No. 0.041;
ive 38; Mismatches 130; Indels 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91817 MW; 9538F2108E787B49 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LDL-RECEPTOR CLASS
LDL-RECEPTOR CLASS
LDL-RECEPTOR CLASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Calcium-binding;
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EGF-LIKE 1.
EGF-LIKE 2.
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VWFC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F5/8 TYPE C.
               or send an email to license@isb-sib.ch)
                                                                                   InterPro; IPR00421; FASB C.
InterPro; IPR00421; FASB C.
InterPro; IPR00219; IDL Feceptor A.
InterPro; IPR00219; IDL Feceptor IPR00219; IDL Feerich.
InterPro; IPR00184; TSPI.
Fam; PF00078; FS F8 LYPE C; I.
Pfam; PF000787; Idl Fecept a; 3.
Pfam; PF00090; FSP II; 4.
Pfam; PF00090; FSP I; 4.
Pfam; PF00090; FSP I; 4.
Pfam; PF00090; FSP I; 4.
SWART; SW0021; FASBC; 1.
SWART; SW0021; IDLa; 3.
SWART; SW00209; TSPI; 4.
                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS01265; FA58C 1; 1.
PROSITE; PS01286; FA58C 2; 1.
PROSITE; PS01209; LDLRA_1; 3.
PROSITE; PS50020; LDLRA_2; 3.
PROSITE; PS50092; TSP1; 4.
PROSITE; PS50199; WPC 2; 1.
OJYCOPTOTEIN; Cell adhesion; Ca.
DOMAIN 29 87 TS1
                                                    EMBL; X93922; CAA63815.1; -.
HSSP; P01130; 1AJJ.
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Best Local Similarity 20.00,
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                                                                                                              376
                                                                                                                                                                       GRIRLLYEDGDSDDDFWCHMWSPLIHPVGWSRRVGHGIXMSE--RRSDMAHHPTFRKIYC 198
                                                                                                                                                                                                                                                    DAVP-YLFKKVRAVYTEGGWFEEGWKLEAIDPLNLGNICVATVCKVLLDGYLMICVDGGP 257
                                                                                                                                                                                                                                                                              326. QAAPKHLFVSQSHSPPPLG-FQVGMKLEAVDRMNPSLVCVASVTDV-VDSRFLVHFDNWD 383
                                                                                                                                                                                                                                                                                                                                      SIDGLDWFCYHASSHAIFPATFCQKNDIELTPPKGY-EAQTFNWENYLEKTKSKAAPSRL 316
                                                                                                                                                                                                                                                                                                                                                                                                                                               DIYPVGWCELTGYQLQPPVA-AEPAT-----PLKAKEATKKKKKQFGKKRKRIP---- 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DT--YDYWC-DPSSPYIHPVGWCQKQEKPLTPPQDYPDPDNFCWEKYLBETGASAVPTWA 440
                                                                                     83 WKGYLMKRLVGSRTLPVDF--HIKMVESMKYPFRQGMRLEVVDKSQVSRTRMAVVDTVIG
                                                                                                                                                                                                                                                                                                                                                                                                                         FINADCPNINGFKVGMKLEAVDLMEPRLICVATVKRVVHRLLSIHFDGWDSEYDQWVDCESP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Ependymocyte,
MEDLINE=96338614; PubMed=8743952;
Gobron S., Monnerie H., Meiniel R., Creveaux I., Lehmann W.,
Lamalle D., Dastugue B., Meiniel A.;
"SCO-spondin: a new member of the thrombospondin family secreted by
the subcommissural organ is a candidate in the modulation of neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Last annotation update)
SCO-spondin (Fragment).
Blos taurus (Bovine).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi,
Mammalia; Butheria; Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47;
           Length 772;
    19.0%; Score 510; DB 1; Length 772; 33.7%; Pred. No. 1.2e-34; Live 53; Mismatches 168; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            560 DGSGHVTGKFTAHHCLSGCPLAER--NÖSRLKAELSDSEASARK 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           867 AA
                                              Matches 136; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9913;
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P98167;
                                                                                                                                                                       141
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SSPO BOVIN
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161 WSPLIHPV----GWSRRVGHGIKMSERRSDMAHHPTFRKIYCDAVPYLFKKVRAVYTEGG 216 --ATFCQKNDIELTPPKGYEAQTFNWENYLEKTKSKAAPSRLFN 318 Repeat; EGF-like domain. 217 WFEEGMKLEAIDPLNLGNICVATVCKVLLDGYLMICVDGGPSTDGLDWFCYHASSHA---370 WAAILRPAPGAPGWS------PVEHADTQGHTPP------PYL-----Gaps

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NCBI_TaxID=9606
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                                                  384
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                        --OAAPSSDAN 490
                                                                          364
                                                                                                                                                                                                                                                                           IPPTKTRPLRQGSKKPLLEDDPQGARKISSEPVPGBIIAVRVKEEHLDVASPDKASSPEL 482
                                                                                                                                                                                                                                                                                                     LDGP-----LRVELLG-CEPAPLCLG----VGHRCVSGECAPRGAPCDGVEDCKDGSD 538
                                                                                                                                                                        SEYDQWYDCESPDIYPVGWCELIGYQLQPPVAAEPAIPLKAKEAIKKKKKOFGK--KRKR 422
                                                                        MDCPNHGFKVGMKLEAVDLMEPRLICVATVKRVVHRLLSIHF--------DGWD
                                                                                                                                                                                                                     ----GCVTPPA-GAGRIESTAWSSAPSSAQPGQLPPQPSEGLAEABADHWHPGRGSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A., Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M., Fritchman J.L., Weidman J.F., Small K.V., Sandesky M., Fuhrmann J.L., Willyon D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M., Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S., Peterson S.N., Smith H.O., Hutchison C.A. III, Vencer J.C.; Science 270:397-403(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -! - SIMILARITY: BELONGS TO THE L29P FAMILY OF RIBOSOMAL PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycoplasma genitalium.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=2097;
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4.3%; Score 116.5; DB 1; Length 2
Best Local Similarity 25.0%; Pred. No. 0.014;
Matches 44; Conservative 38; Mismatches 65; Indels
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200 UNKNOWN.
23258 MW; 5BC115E52AASEA92 CRC64;
: | | : : | | : : | 446 APQLFPKNWNGPSTVWMFARMVQARHVRVWPSDGHH--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Sos ribosomal protein L29.
RPMC OR RPL29 OR MG159.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         200 AA
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InterPro; IPR001854; Ribosemal L29.
Pfam, PF00831; Ribosemal L29; 1.
TIGRFAMS; TIGR00012; L29; 1.
PROSITE; PS00579; RIBOSOMAL L29; 1.
Ribosemal protein; Complete Proteome.
DOMAIN
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STRAIN=ATCC 33530 / G-37;
MEDLINE=96026346; PubMed=7569993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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MYCGE
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331 KLEAVDLMEPRLICVATVKRVVHRLLSIHFD---GWDSEYDQW--VDCESPDIYPVGW-- 383

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                                                                                                                           90 KLSTKPESKQETKKAEVKPKVESKPESKQETKKAEVKPLKQETKKVEVKPKVEPKPLKQE 149
32 KLAHGELDKPHLI--AKVRKLLAVVLTILTERKLNWQVEKDKYKLLSRKTNELIVNSWKQ 89
                                                                         -----CELTGYQLQPPVAAEPATPLKAKEATKKKKQFGKKRKIPPTKTRPLRQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Raff J.W.;
"The TACC domain identifies a family of centrosomal proteins that can
                                                                                                                                                                                                                             435 SKKPLLEDDPQGARKISSEPVPGEIIAVRVKEEHLDVASPDKASSPELPVSVENIK 490
                                                                                                                                                                                                                                                                           : | | : | : | : | : | : | 1. | : | | 1. | | 1. | | 1. | | 1. | | 1. | | 1. | | 1. | | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 1. | 
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-!- FUNCTION: MAY PLAY A ROLE IN ORGANIZING CENTROSCOMAL MICROTUBULES.
MAY ACT AS A TUMOR SUPPRESSOR PROTEIN. MAY REPRESENT A TUMOR
PROGRESSION MARKER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 44-1026 FROM N.A. (ISOFORM 3).
Pu J., Li C., Rodriguez M., Banerjee D.;
"Expression of TACC2 protein mRNA in human microvascular endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20214826; PubMed=10749935;
Chen H.-M., Schmeichel K.L., Mian I.S., Lelievre S., Petersen O.W.,
Bissell M.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       candidate breast tumor suppressor and biomarker for tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAC2_HUMAN STANDARD; PRT; 1026 AA.
095359; Q9NZ41; Q9NRS;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 44, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Transforming acidic coiled-coil-containing protein 2 (Anti Zuai-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gergely F., Karlsson C., Still I.H., Cowell J.K., Kilmartin J., Raff J.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBUNIT: INTERACTS WITH MICROTUBULES.
-!- SUBCELLUTAR LOCATION: NUCLEAR; CONCENTRATED AT CENTROSOMES.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for some
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Comment=Experimental confirmation may be lacking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isold=095359-2; Sequence=VSP_006368, VSP_006369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 97:14352-14357(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 1).
TISSUE=Brain, Fetal brain, and Skeletal muscle;
MEDLINE=20570483; PubMed=11121038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 375-1026 FROM N.A. (ISOFORM 2).
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Genomics 2:249-256(1988).
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                                                                                                                                                                                                                                                                 253 VDGGPSTDGLDWFCYHASSHAIFPATFCQKNDIELTPPKGYEAQTFNWENYLEKTKSKAA 312
                                                                                                                                                                                                                                                                                  77 VPDGPRSDSVBGSPFRPPSHS-FSAVFDEDKPIASSGTYNLDFDNIBLVDTFQTLEPRAS 135
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COLLED COIL (POTENTIAL).
COLLED COIL (POTENTIAL).
Missing (in leoform 2).
/FTid=VSP 006368.
Missing (in lsoform 2 and isoform 3).
/FTid=VSP 006369.
PAPPEPPEPVIPEPRVSTQPPPEE -> MFWYKRGAPMRP
                                                                                                                                                                                                                                                                                                                                                                                                 424 PPTKTRPLROGSKKPLLEDDPQGARKISSEPVP-GELIAVRVKEEHLDVASPDKASSPEL 482
                                                                                                                                                                                                                                                                                                                                                                                                                      222 - PTETPPVKETOQEP----DEESL-----VPSGENLASETKTESAKTEGPSPALLEET 269
                                                                                                                                                                                                                                                                                                            313 PSRLFNMDCPNHGFKVGMKLEAVDLMEPRLICVATVKRVVHRLLSIH----FDGWDSEYDQ
                                                                                                                                                                                                                                                                                                                                                     370 WVDCESPDIYPVGWCELTGYQLQPPVAAEPATPLKAKEATKK-----KKKQFGKKRKRI
                                                                                                                                                                                                                                                                                                                                                                    57; Gaps
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Zeviani M., Darras B.T., Rizzuto R., Salviati G., Betto R.,
Bonilla E., Miranda A.F., Du J., Samitt C., Dickson G., Walsh F.S.,
Dimauro S., Francke U., Schon E.A.;
"Cloning and expression of human nebulin cDNAs and assignment of the
gene to chromosome 2q31-q32.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Labeit S., Kolmerer B.; "The complete primary structure of human nebulin and its correlation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                     4.1%; Score 109.5; DB 1; Length 1026; 23.6%; Pred. No. 0.47; ative 33; Mismatches 95; Indels 57;
                                                                                                                                                                                      VSVIDGVVCVS (IN REF. 3).
1026 AA; 112110 MW; E2575FCB446E9CF8 CRC64;
EMBL; AF095791; AAC64968.2; -.
EMBL; AF176646; AAF63433.1; ALT_INIT.
EMBL; AF220152; AAF29537.2; -.
EMBL; AF00152; AAF29537.2; -.
MIM; 605302; -.
GO; GO:0007048; P:oncogenesis; TAS.
Fam; PF05010; TACC; 1.
Coiled coll; Valear protein; Alternative splicing.
DOMAIN 43 51 POLY-PRO.
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01-FEB-1991 (Rel. 17, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=95257391; PubMed=7739042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  muscle structure.";
Mol. Biol. 248:308-315(1995).
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                                                                                                                                                                                                                                           57; Conservative
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THE STRUCTURE BY NAME OF 6610-6669.

THE STRUCTURAL INTEGRITY OF SARCOMERES AND THE MEMBRANE SYSTEM ASSOCIATED WITH THE MYOFIBRILS. BIND AND STABILIZE F-ACTIN.

THE STRUCTURAL INTEGRITY OF SARCOMERES AND THE MEMBRANE SYSTEM ASSOCIATED WITH THE MYOFIBRILS. BIND AND STABILIZE F-ACTIN.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R GO; GO:0015629; C:actin cytoskeleton; TAS.
R GO; GO:0015629; C:actin cytoskeleton; TAS.
R GO; GO:00030017; C:sarcomere; NAS.
R GO; GO:00031017; E:sequelation of actin thin filament length ac...;
R GO; GO:0003107; F:regulation of actin thin filament length ac...;
R GO; GO:0003107; F:regulation of actin thin filament length ac...;
R GO; GO:00003107; F:regulation of actin thin filament length ac...;
R InterPro: IPR007525; P:somatic muscle development; NAS.
R InterPro: IPR001452; SH3.
R PFEM; PFO0880; Nebulin; 146.
R PFEM; PFO0018; SH3; I.
R PRINTS; PR00452; SH3: All R PFEM; PFO00066; SH3; I.
R PFEM; PFO00066; SH3; I.
R PRODOUG66; SH3; I.
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NEBULIN 9.
NEBULIN 10
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EMBL; M19668; AAA5916.1; ALT_SEQ.
EMBL; M19668; AAA5917.1; ALT_SEQ.
PIR; S55024; S55024.
PDB; 1ARK; 28-JAN-98.
PDB; INEB; 24-DEC-97.
Genew; HGNC:7720; NEB.
MIM; 161650; -.
MIM; 256030; -.
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REPEAT         3603         MEBULIN         99.           REPEAT         3636         NEBULIN         100.           REPEAT         3701         NEBULIN         100.           REPEAT         3702         NEBULIN         100.           REPEAT         3780         3810         NEBULIN         100.           REPEAT         3780         3810         NEBULIN         100.           REPEAT         3846         3876         NEBULIN         100.           REPEAT         3846         3876         NEBULIN         100.           REPEAT         3944         NEBULIN         100.           REPEAT         4014         NEBULIN         100.           REPEAT         4021         4024         NEBULIN         110.           REPEAT         4024         NEBULIN         111.         NEBULIN         111.           REPEAT         4156         NEBULIN         112.         NEBULIN         114.           REPEAT         420         NEBULIN         117.         REPEAT         420         NEBULIN         117.           REPEAT         430         NEBULIN         120.         NEBULIN         120.           REP	Query Match Best Local Similarity 19.6%; Pred. No. 17; Matches 72; Conservative 54; Mismatches 100; Indels 142; Gaps 19;	160 MWSPLIHPVGWSRRVGHGIKMSERRSDMAHHPTFRKI 196 ::  :::  :	197 YCDAVPYLFKKVRAVYTEGGWFEEGMKLEAIDPLNLGNICVATVCKVLLDGYL 249 2326 QDDPKLVLSMNVAKMQSEREYKKDFEKWKTKFSSPVDMLGVVLAKKQELVSDVDYKNYL 2385	250 MICVDGGPSTDGLDWFCYHASSHAIFPATFCQKNDIELTPPKGYEAQTFN 299 2386 HQWTCLPDQNDV-VQAKKYYELQSENLYKSDLEWLR 2420	300WENYLEKTKSKAAPSRLFNMDCPNHGFKVGMKLEAVDLMEPRL 342	343 ICVATVKRVVHRILSIHPDGWDSEYDQ-WVDCESPDIYPVGWCEL- 386 : : :     : :	387 -TGYQLQPPVAAEPATFLKAKEATKKKKKQFGKKRKRIPPTKTRPLRQGSKKPL 439	440LEDDPQ 445        2566 RNIEDDPK 2573	FULL 8 P. BOVIN P. PAP BOVIN P. STANDARD; PRT; 738 AA. P25500; 01-MAY-1992 (Rel. 22, Created) 01-FEB-1994 (Rel. 28, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) POLY(A) POLYMERASE alpha (EC 2.7.7.19) (PAP) (Polynucleotide adenylyltransferase alpha). BAPOLA OR PAP. Bos taurus (Bovine).
		\$ g	Q qq	& a	중 염	, Q	<i>장</i> 웜	P &	RESULT PAP_BOY ID PAP AC P2 AC 01 DT 01 DT 02 DE P0 DE P0 CR AC AC CR AC

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Crystal structure of mammalian poly(A) polymerase in complex with an analog of ATP".

EMBO J. 19:4193-4203 (2000).

-!- FUNCTION: Polymerase that creates the 3' poly(A) tail of mRNA's.

Also required for the endorshbonucleolytic cleavage reaction at some polyadenylylation sites. May acquire specificity through interaction with a cleavage and polyadenylation specificity factor (CRF) at its C-terminus.

-!- CATALYMIC ACTULITY: N ATP + (nucleotide)(M) = N diphosphate + (nucleotide)(M+N).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
MBDLINE=20460225; Unbmed=10944102;
Martin G., Keller W., Doublie S.;
"Crystal structure of mammalian poly(A) polymerase in complex with an
                                                                                                              TISSUE=Thymus;
MEDLINE=92097545; PubMed=1756732;
Wahle E., Martin G., Schiltz E., Keller W.;
"Isolation and expression of cDNA clones encoding mammalian poly(A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=Short;
Isold=P25500-2; Sequence=VSP 004524, VSP 004525, VSP 004526;
Isold=P25500-2; Sequence=VSP 004524, VSP 004525, VSP 004526;
Note PTM: Phosphorylated phosphorylation/dephosphorylation may regulate the interaction between PAP and CPSF.
SIMILARITY: BELONGS TO THE POLY(A) POLYMERASE FAMILY.
                      Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-96221320; PubMed=8665867;
Martin G., Keller W.;
"Mutational analysis of mammalian poly(A) polymerase identifies a region for primer binding and catalytic domain, homologous to the family X polymerases, and to other nucleotidyltransferases.";
EMBO J. 15:2593-2603(1996).
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND SEQUENCE OF 96-102 AND 444-467.

TISSUE=Heart muscle;
MEDLINE=91375535; PubMed=1896071;
MEDLINE=91375535; PubMed=1896071;
"Prinary structure and expression of bovine poly(A) polymerase.";
Nature 353:229-234(1991).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                           SEQUENCE FROM N.A., AND SEQUENCE OF 1-20; 206-254 AND 385-396
                                                                                                                                                                                                                                                                     Wahle E.;
Submitted (AUG-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=Long;
IsoId=P25500-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAINS, ACTIVE SITES, AND MUTAGENESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X61585; CAA43782.1; -.
EMBL; X63436; CAA45031.1; -.
EDBL; 1FSA; 13-58P-00.
InterPro; IPR002934; NIP transf.
InterPro; IPR001201; PAP_25A_core.
InterPro; IPR007012; PAP_CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: Monomer.
SUBCELLULAR LOCATION: Nuclear.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                              EMBÔ J. 10:4251-4257(1991).
                      Mammalia, Eutheria, Ce
Bovidae, Bovinae, Bos.
                                                         NCBI TaxID=9913
                                                                                                                                                                                                polymerase."
                                                                                                                                                                                                                                                     REVISIONS.
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Pfam; PP01909; NTP transf 2; 1.
Pfam; PP01909; NTP transf 2; 1.
Pfam; PP04926; NTP transf 2; 1.
Pfam; PP04926; PAP central; 1.
Pfam; PP04926; PAP central; 1.
NNCHA processing; Transferase; Transcription; RNA-binding; NNCHEAT protein; Phosphorylation; Alternative splicing; 3D-structure.

ACT SITE 112 112
ACT SITE 114 114
ACT SITE 166 166
NUCLEAR LOCALIZATION SIGNAR, 1
                                                                            NUCLEAR LOCALIZATION SIGNAL 1.
                                                                                           Missing (in isoform Short).
/FTG-VSP 004524.
KT -> II (in isoform Short).
/FTIG-VSP 004525.
Missing (in isoform Short).
/FTIG-VSP 004526.
S -> R (IN REF. 3).
                                                     1112
1114
1166
1166
658
682
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162
171
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191
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VARSPLIC
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isoform 4)
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AB086637 BAC00966.1, JOHNED.
AB086639 BAC00996.1, JOHNED.
AB086640 BAC00996.1, JOHNED.
AB086641 BAC00996.1, JOHNED.
AB086641 BAC00996.1, JOHNED.
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AB086633, BAC00996.1, JOINED
AB086634, BAC00996.1, JOINED
AB086635, BAC00996.1, JOINED
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InterPro; IPR002934; NTP_transf.
InterPro; IPR001201; PAP_25A core.
InterPro; IPR007012; PAP_centr.
InterPro; IPR007010; PAP_RNA_bind.
Pfam; PP04926; PAP_RNA-bind; I.
                                                                                                                                                                                                                                                                                                                    EMBL; U52197; AAC52586.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
 274 IFPATECOKN-DIELTPPKGYEAQTFNWENYLEKTKSKAAPSRLFNMDCPNHGFKVGMKL 332
                                                                                                                                                                                                                       441 VFKKTENSENLSVDLT----YDIQSFTDTVYRQAINSKM-------FEVDMKI 482
                                                                                                                                                                                                                                              333 BAVDLMEPRLICVATVKRVVHRLLSIHF-----DGW-----DSEYDQWVDCESPD 377
                                                                                                                                                                                                                                                             378 IYPVGWCELTGYQLQ-----PPVAAEPATPLKAKEAT----KKKKKQFGKKRK 421
                                                                                                                                                                                                                                                                                                             533 SVPSPTSAMKTSPLNSSGSSQGRNSPAPAVTAASVTNIQATEVSLPQINSSESSGGTSSE 592
                                                                                                                                                                                                                                                                                                                                           RIPPTKTRPLRQGSKKPLLEDDPQGARKISSEPVPGEIIAVRVKEEHLDVASPDKASSPE 481
                                                                                                                                                                                                                                                                                                                                                           593 SIPQTATQPAISSPPKPTVSRVVSSTRLVNPPPRPSGNAAAKIPN---PIVGVKRTSSPH 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: Polymerase that creates the 3' poly(A) tail of mRNA's. Also required for the endoribonucleolytic cleavage reaction at some polyadenylylation sites. May acquire specificity through interaction with a cleavage and polyadenylation specificity factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Brain;
MEDLINE=96189120; PubMed=8628305;
Zhao W., Manley J.L.;
"Complex alternative RNA processing generates an unexpected diversity
                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kashiwabara S., Noguchi J., Zhuang T., Ohmura K., Honda A., Sugiura S., Miyamoto K., Takahashi S., Inoue K., Ogura A., Baba T.; "Regulation of spermatogenesis by testis-specific, cytoplasmic Science 298:1999-2002(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                         AC G61183; Q61208; Q81209; Q844X2;
DT 28-FEB-2003 (Rel. 41, Created)
DT 15-SEP-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Poly(R) polymerase alpha (EC 2.7.7.19) (PAP) (Polymucleotide adenylyltransferase)
N PAPOLA OR PAP OR PLAP.
S Mus musculus (Mouse)
                                                                                                                                                                          63;
                                                                                                                                                  3.7%; Score 98.5; DB 1; Length 738; 20.9%; Pred. No. 2.5; cive 33; Mismatches 105; Indels 63
                                                                                                                             82310 MW; DOB90662F89363E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORMS 2; 3 AND 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       poly(A) polymerase isoforms.";
1. Cell. Biol. 16:2378-2386(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=129/SvJ;
MEDLINE=22359775; Pubmed=12471261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                         482 LPVSVENIKQETDD 495
                                                                                                                                                                                                                                                                                                                                                                                                                650 KEESPKKTKTEEDE 663
                                                                                                                                                                           Conservative
                                                                              479
488
491
                                                                                                                493
738 AA;
                                                                                                                                                              Similarity
                                                                                                                                                                        53;
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                                                                                                                             SEQUENCE
                                                                                                                                                   Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                Name=3; Synonyms=V;
IsoId=Q61183-3; Sequence=VSP_004529, VSP_004530;
Name=4; Synonyms=VI;
IsoId=Q61183-4; Sequence=VSP_004527, VSP_004528;
PTM: Phosphorylated. Phosphorylation/dephosphorylation may regulate the interaction between PAP and CPSF (By similarity).
SIMILARITY: BELONGS TO THE POLY(A) POLYMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA processing Transferage, Transcription, RNA-binding, blosphorylation; Nuclear protein; Alternative splicing.

INT MET 112 112 BY SIMILARITY.

ACT SITE 114 114 BY SIMILARITY.

ACT SITE 166 BY SIMILARITY.

ACT SITE 166 BY SIMILARITY.

VARSPLIC 279 292 EWPNPVLIKQPEEC -> YVFRLYYNKIDCRH (in
(CPSF) at its C-terminus (By similarity).
CATALYTIC ACTIVITY: N ATP + {nucleotide}(M) = N diphosphate {nucleotide}(M+R)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /Fridavsp 004529.
Missing (In isoform 3).
/Fridavsp 004530.
/Fridavsp 004531.
                                                                                                                                                                                                                                                                                                                          Name=2; Synonyms=III;
IsoId=061183-2; Sequence=VSP_004531, VSP_004532;
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                                                                                                      -!- SUBUNIT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
-!- ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        004527.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              274 IFPATFCOKN-DIELTPPKGYEAQTFNWENYLEKTKSKAAPSRLFNMDCPNHGFKVGMKL 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---DGW-----DSEYDQWVDCESPD 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            378 IYPVGWCELTGYQLQ-----PPVAAEPATPLKAKEAT----KKKKKQFGKKRK 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    422 RIPPTKTRPLRQGSKKPLLEDDPQGARKISSEPVPGEIIAVRVKEEHLDV---ASPDKAS 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2198 HUMAN STANDARD; PRT; 1377 AA.
QUENGY; 043212; 043434; 060898; Q9H538; Q9UEU2;
28-FEB-2003 [Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last equence update)
28-FEB-2003 (Rel. 41, Last annotation update)
210-FEB-2003 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-98384238; PubMed-9716603; Reiter A., Sohal J., Kulkarni S., Chase A., Macdonald D.H.C., Apular R.C.T., Goncalves C., Hernandez J.M., Jennings B.A., Goldman J.M., Cross N.C.P.; "Consistent flusion of ZNP198 to the fibroblast growth factor receptor-1 in the t(8.13) (p11,q12) myeloproliferative syndrome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                             SVPSPTSAMKTSPLNSSGSSQGRNSPAPAVTAASVTSIQASEVSVPQANSSESPGGPSSE
                                                                                                                                                                                                                                                                                                              Gaps
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MEDIINE=99107818; PubMed=9889006;
Kulkarni S., Reiter A.J., Smedley D., Goldman J.M., Cross N.C.P.;
"The genomic structure of ZNF198 and location of breakpoints in the t(8;13) myeloproliferative syndrome.";
Genomics 55:118-121(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98245146; PubMed=9576949;
Popovici C., Adelaide J., Ollendorff V., Chaffanet M., Guasch G., Jaczot M., Leroux D., Birnbaum D., Pebusque M.-J.;
Fibroblast growth factor receptor I is fused to FIM in stem-cell myeloproliferative disorder with t(8:13) (pi2;q12).";
Proc. Natl. Acad. Sci. U.S.A. 95:5712-5717(1998).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NOBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                          69;
                                                                                                                                                                                                               DB 1; Length 738;
                                                                                                                                                                                                                                                                                                     Indels
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Blakey S., Wall M.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
[5]
                                        /FTId=VSP 004532.
K -> L (IN REF. 1):
168E8757143EF1F6 CRC64;
         Missing (in isoform 2).
                                                                                                                                                                                                                                                                                                     . 66
                                                                                                                                                                                                                                                             2.5;
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                                                                                                                                                                                                                                                                                                     34; Mismatches
                                                                                                                                                                                                               3.7%; Score 98.5;
21.4%; Pred. No. 2.9
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82177 MW;
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738
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738 AA;
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375
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leukaemia/Jymphoma syndrome.";

Nat. Genet. 18:84-87(1998).

Nat. Genet. 18:84-87(1998).

-! FUNCTION: May function as a transcription factor.

-! FUNCTION: May function as a transcription factor.

-! SUBCELLULAR LOCATION: Nuclear (Potential).

-! DISBABE: Involves FORTI AND ENFISE. The resulting transcript is a which involves FORTI AND ENFISE. The resulting transcript is a possible candidate for stem cell leukemia lymphoma syndrome/SCLL.

-! SIMILARITY: Contains 5 MYM-type zinc fingers.

-! SIMILARITY: Contains 5 MYM-type zinc fingers.

-! CAUTION: Ref. 5 sequence differs from that shown due to a frameshift in position 330.

-! CAUTION: Ref. 6 sequence differs from that shown due to frameshifts

-! DATABASE: NAME-Aklas Genet. Cytogenet. Oncol. Haematol.;

WWW="http://www.infobiogen.fr/services/chromcancer/Genes/ZNF198ID114.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
SEQUENCE OF 152-1377 FROM N.A.
MEDILIE=99361795; Pubmed=9694738;
Still I.H., Cowell J.K.;
"The t (8,13) atypical myeloproliferative disorder: further analysis of
the ZRF198 gene and lack of evidence for multiple genes disrupted on
chromosome 13.";
                                                                                                                                                                                                                                                                                                  SEQUENCE OF 621-1377 FROM N.A.
MEDLINE-98085877; PubMed=9425908;
Aiao S., Nalabolu S.R., Aster J.C., Ma J., Abruzzo L., Jaffe E.S.,
Stone R., Weissman S.M., Hudson T.J., Fletcher J.A.;
"FGFR1 is fused with a novel zinc-finger gene, ZNF198, in the t(8;13)
                                                                                                                                                                               Warren W., Abdul-Rauf M., Somers
                                                                                                                                                                           Smedley D., Hamoudi R., Clark J., Warren W., Abdul-Rauf M., Somers Venter D., Fagan K., Cooper C., Shipley J.;
"The t(8;13) (p11;q11-12) rearrangement associated with an atypical myeloproliferative disorder fuses the fibroblast growth factor receptor 1 gene to a novel gene RAMP.";
Hum. Mol. Genet. 7:637-642 (1998).
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MEDLINE=98167848; PubMed=9499416;
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                                                                                                         Blood 92:1456-1458(1998)
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"Isolation and characterization of two homologous cDNA clones from
                      Torpedo electromotor neurons.";
DNA 8:555-561(1989).
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721 AA;
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DT 15-JUL-1998 (

DT 18-JUL-1998 (

DT 28-FEB-2003 (
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                                                                                                                                                                                                                                                                          -> GWLKWIQV
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                                          Gaps
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01-JAN-1990 (Rel. 13, Last sequence update)
01-JAN-1990 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last amnotation update)
Electromotor neuron-associated protein 1 (Fragment).
Torpedo californica (Pacific electric ray).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Chondrichthyes;
Elasmobranchii; Squalea, Hypnosqualea; Pristiorajea; Batoidea;
Torpediniformes; Torpedinoidei; Torpedinidae; Torpedo.
                                                                                                              MYM-TYPE 1 (POTENTIAL).
MYM-TYPE 2 (POTENTIAL).
MYM-TYPE 3 (POTENTIAL).
MYM-TYPE 4 (POTENTIAL).
MYM-TYPE 5 (POTENTIAL).
BREAKPOINT FOR TRANSLOCATION TO FORM
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SPSRNSVVTSCLISLMKNNRILL (IN REF. 1)
NW -> ASL (IN REF. 4).
K -> G (IN REF. 1).
MISSING (IN REF. 6).
MISSING (IN REF. 6).
DF -> IS (IN REF. 6).
MISSING (IN REF. 6).
MISSING (IN REF. 6).
MISSING (IN REF. 6).
MISSING (IN REF. 6).
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20.2%; Pred. No. 8.4;
iive 46; Mismatches 147; Indels 103;
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Ngsee J.K., Scheller R.H.;
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1377 AA; 154910 M
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993 SSMPDVPYEPD 1003
                      Genew, HGNC:12989; ZNF198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              273 AIFPATFCOKNDIELTPPKGYEAQ-TFNWENYLEKTKS----KAAPSR-----LFNMDC
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                                        ORGANELLES.
-1- MISCELLANDOUS: HAS A HIGHLY BASIC REGION WITH MANY COPIES OF THE SEQUENCE KKE, REPEATED BUT NOT AT FIXED INTERVALS.
-1- SIMILARITY: TO ELECTROMOTOR NEURON-ASSOCIATED FROTEIN 2.
-!- SUBCELLULAR LOCATION: ASSOCIATED WITH MEMBRANES OF INTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 721;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 X 3 AA APPROXIMATE REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.6%; Score 95.5; DB 1; Length 7; 22.2%; Pred. No. 4.3; .ve 45; Mismatches 112; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        721
81241 MW; B53E69A9F309CE00 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLU/LYS-RICH (BASIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   465 -- KEEHLDV----ASPDKASSPELPVSVENIKOE 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        664 EKKKEEKDVKKESAKPDRKEEKAV-IKKEKVKKE 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
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343 ERDIYPRRWGLGPIAQKKKQMKADGKLDKYGR-VNENTPENWKKDYKDL-DEQPAPPIPE 400
                                                                                             401 SKLVAPBPQLPKKKSLIEEVEVDIDVEDKSEKKEKKDKKEKKEKKDKKEKKEKKEKKKOKKEKK 460
                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
ADAWTS-12 precursor (EC 3-4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 12) (ADAM-TS 12) (ADAM-TS12).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE.
PTM: IS SUBJECTED TO AN INTRACELLILAR MATURATION PROCESS LEADIND
FOR A FRAGMENT CONTAINING THE N-TERMINAL REGION INCLUDING THE
METALLOPROTEINASE, DISTUTEGRIN-LIKE, CYS-RICH AND TS-1 DOMAINS AND
THE C-TERMINAL FRAGMENT CONTAINING THE SPACER 2 AND THE FOUR IS-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMÁIN: THE SPACER DOMAIN AND THE TSP TYPE 1 DOMAINS ARE IMPORTANT
FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----KEATKKKKKOFGKKRKRIPPTKTRPLROGSKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        matrix (By similarity).
-!- TISSUE SPECIFICITY: Expressed exclusively in fetal lung. Is wic expressed in gastric carcinomas and in cancer cells of diverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- SIMILARITY: Belongs to peptidase family M12B.
-i- SIMILARITY: Contains I disintegrin-like domain.
-i- SIMILARITY: Contains I PLAC domain.
-i- SIMILARITY: Contains 8 TSP type-1 domains.
                                                                                                                                                                                                                                                                                                                        PRT; 1593 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR002870; Pep_M12B_propep
IPR001590; Reprolysin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Petal lung;
MEDLINE=21264577; PubMed=11279086;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nterbro; IPR006025; Zn MTpeptdae.
fam; PF01562; Pep_M12B_propep; 1.
fam; PF01421; Reprolysin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro, IPR001762; Disintegrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AJ250725; CAC20419.1;
Genew; HGNC:14605; ADAMTS12.
                                                                                                                                               438 PLLEDDPQGARK 449
                                                                                                                                                                                              461 RKAEDDSSKSEK 472
                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF00090; tsp_1; 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIM; 606184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         origin.
                                                                                                                                                                                                                                                                                                                        AT12 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interPro;
                                                 395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the between abioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                221 RSG-AMSESDNIVTLHDVL----DA-QYVYDNTR-----DESYLRKIIQPL--- 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 295 AQTFNWENYLEKTKSKAAPSRLFNMDCPNHGFKVGM-KLEAVDLMEPRLICVATVKR--- 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----IAIGIAQMSTVDLQSCDHGIVAKVKRCIM 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ICVATVCKVLLDGYLMICVDGGPSTDGLDWFCYHASSHAIFPATFCQKNDIELTPPKGYE 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----ESLLVGYKRVVV----KDSAVNSVCYGAK--LMIÞGLLRYEBGIEL-----YD 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----VVHRLLSIHFDGWDSEYDQWVDCESPDIYPVGWCELTGYQLQPP--- 394
Jentromere/microtubule binding protein CBF5 (Centromere-binding factor
) (Nucleolar protein CBF5).
                                                                                                                                                                                                                                                                                                                        BE IN
                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY).
SUBCELLULAR LOCATION: Nuclear; nucleolar (By similarity).
SIMILARITY: BELONGS TO THE TRUB FAMILY OF PSEUDOURIDINE SYNTHASES.
SIMILARITY: Contains 1 PUA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GHGIKMSERRSDMAHHPTFRKIYCDAVPYLFKKVRAVYTEGGWFEEGMKLEAIDPLNLGN
                                                                                                                                                                                                                                                                       IT IS A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42 NDASHDFWCNLGTVDVHPIGWCAINSKILVPPRTIHAKFTDWKGYLMKRLVGSRTLPVDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NPSSHEV------GTLDPKVTGCLIVCIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 HIKMVESMKYPFRQGMRLEVV-----DKSQVSRTRMAVVDTVIGG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               110 ATRLVKS-----QQGAGKEYVCIVRLHEQLKDDKELNR----ALENLTGALFQRPPLISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----REVELLYEDGDSDDD-----FWC-----HMWSPLIH----PVGWS----RRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               161 VKRQLRVRTVYDSKLIBFDNKRGLGVFWASCBAGTYWRTLCVHLGMLLGVGGHMQELRRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 173; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U59149; AAB94297.1; -.

R InterPro; IPR0044802; CDf5.

R InterPro; IPR004518; PUA.

R InterPro; IPR004521; Unchar_dom_2.

R InterPro; IPR004521; Unchar_dom_2.

R Pfam; PF01472; PUA; 1.

R Pfam; PF01509; TruB_N; 1.

R SMART; SM00359; PUA; 1.

R TIGRFAMS; TIGR00425; CBF5; 1.

R TIGRFAMS; TIGR00451; unchar_dom_2; 1.

R PROSITE; PS5089; PUA; 1.

Microtubules; Centromers; Repeat; Nuclear protein; DNA-binding.

T DOMAIN 267 342.
                                                                                                                                                                                   SEQUENCE FROM N.A.
Jiang W., Clifford J., Koltin Y.;
Submitted (JAN-1198) to the EMBL/Genbank/DDBJ databases.
-!- FUNCTION BINDS IN VITRO TO CENTROMERES AND MICROTUBULES. IT I CENTROMERE DNA-CBF3-BINDING FACTOR AND IS INVOLVED IN MITOTIC CENTROMERE DNA-CBF3-BINDING FACTOR AND IS INVOLVED IN MITOTIC CHROMOSOME SEGREGATION. IT IS ESSENTIAL FOR CELL GROWTH. MAY B SOME WAY ASSOCIATED WITH THE CBF3 110 KDa SUBUNIT (CBF3A) (BY
                                                                                             Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54321 MW; 3BAF5104E12C9EB6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.4%; Score 92.5; DB 1; 1
20.9%; Pred. No. 4.4;
tive 61; Mismatches 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----EVVLMTTKGEA
                                                                      Candida albicans (Yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                479 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                               NCBI_TaxID=5476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  351
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540 IDGQFSEKMLDAVIDGTPCFEGGNSRNVCINGICKAVGCDYE---IDSNATEDRCGVCLG 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HASSHAIFPATFCOKN----DIELTPPKGYEAQTFNWE---NYLEKTKSKAAPSRLFNM
                                                                         DGSSCOTVRKMFKOKEGSGYVDIGLIPKGARDIRVMEIEGAGNFLAIRSED--PEKYY--
                                                                                                                                          --LNGGF11QWNGNYKLAGTVFQYDRKGDLEKLMATGPTNESVW1QLLFQVTNPG1KYEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     392 OPPVAAEP--ATPLKAKEATKKK-----KKOFGKKRKRIPPTKTRPLROGSK-KPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                    Zea mays (Maize).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=cv. W22;
MEDLINE=91227140; PubMed=1709276;
MEDLINE=91227140; PubMed=1709276;
MEDLINE=91227140; Chaubet N., Philipps G., Gigot C.;
"Nucleotide sequence and expression of a maize H1 histone cDNA.";
Nucleic Acids Res. 19:1491-1496(1991).
-!- FUNCTION: HISTORES H1 ARE NECESSARY FOR THE CONDENSATION OF
NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.4%; Score 91.5; DB 1; Length 245; 33.3%; Pred. No. 2.2; tive 12; Mismatches 37; Indels 1
                                                                                                            DCPNHGFKV----GMKLEAVDL-----MEPRLICVATVKRVVHRLL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D1FD73DAA74A6778 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASP/GLU-RICH (ACIDIC)
ARG/LYS-RICH (BASIC).
GLOBULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chromosomal protein; Nuclear protein; DNA-binding.

INIT MET 0 0 ASP/GLU-RICH (ACIDIC)

DOMAIN 31 45 ARG/LYS-RICH (RASIC)
                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                       245
                                                                                                                                                                                                        811 TİQKDĞLDNDVEQMYFWQYGHWTEC 835
                                                                                                                                                                           SIHFDGWDS-----EYDQWVDC 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR005818; Histone H1/H5.
InterPro; IPR005819; Histone H5.
InterPro; IPR003216; Linkerhist N.
Pfan; PF00538; linker histone; I.
PRINTS; PR00624; HISTONEHS.
ProDom; PD000373; Linkerhist N; 1.
SWART; SM00526; H15; 1.
                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25217 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X57077; CAA40362.1; -. PIR; S26826; S26826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                  01-NOV-1991 (Rel. 20, C. 01-NOV-1991 (Rel. 20, Li. 15-JUL-1999 (Rel. 38, Li. Histone H1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          245 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; S26826; S2e
MaizeDB; 25540;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                     H1 MAIZE
P23444;
                                              268
                                                                                                            320
                                                                                                                                          753
                                                                                                                                                                             357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                            RESULT 14
                                                                                                                                                                                                                                                                           MAIZE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            434 KCSEEYI-----TRFLDRGW-GFCLDDI--------PKKKGLKSKV 465
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59; Mismatches 166; Indels 187; Gaps
          PROSITE; PSS0215; ALAM MEPRO; 1.
PROSITE; PS00546; CYSTĒINE SWITCH; FALSE NEG.
PROSITE; PS00546; CYSTĒINE SWITCH; FALSE NEG.
PROSITE; PS00514; DISINTEGRIN_2; FALSE_NEG.
PROSITE; PS50014; DISINTEGRIN_2; FALSE_NEG.
PROSITE; PS00142; ZINC_PROTEASE; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
PROSITE; EXACALIDOTOTEASE; 2inc; Signal; Glycoprotein; Zymogen; Sepact; Extracallular matrix.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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SEQUENCE FROM N.A.

SEQUENCE STRAIN=S286C / AB972;

MEDINE=97313271; PubMed=9169875;

Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V.,

A Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V.,

A Chung E., Churcher C.M., Coster F., Davis K., Charry J.M.,

Dietrich F.S., Delius H., DiPaolo T., Dubois E., Duesterhoeft A.,

Dietrich F.S., Delius H., DiPaolo T., Dubois E., Duesterhoeft A.,

Dietrich F.S., Delius H., DiPaolo T., Dubois E., Duesterhoeft A.,

Dietrich F.S., Delius H., DiPaolo T., Dubois E., Duesterhoeft A.,

A Hall J., Hebling U., Heumann K., Hibbert H., Hillier L.,

Hunicke-Smith S., Hyman R., Johnston M., Kalman S., Kleine K.,

A Komp C., Kunfi O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J.,

A Marathe R., Messenguy F., Mewes H.-W., Mittipati S., Moestl D.,

Mueller-Auer S., Namath A., Nentwich U., Oeffner P., Pearson D.,

Petel F.X., Pohl T.W., Purnelle D., Schäfer M., Scharfe M.,

Scherens B., Schramm S., Schroeder M., Sdicu A.M., Tettelin H.,

Urrestarazu L.A., Ushinsky S., Vierendeels F., Vissers S., Voss H.,

Walsh S.V., Wambutt R., Wang Y., Wedler E., Wedler H., Winnett E.,

A Zhong W.W., Zollner A., Vo D.H., Hani J.;

Nature 387:103-105 (1997).
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Eisen A., Utley.R.T., Nourani A., Allard S., Schmidt P., Lane W.S., Lucchesi J.C., Cote J.;
"The yeast NuA4 and Drosophila MSL complexes contain homologous subunits important for transcriptional regulation.";
J. Biol. Chem. 276:3483-3491(2000).
-!- FUNCTION: MAY PLAY A ROLE IN TRANSCRIPTION REGULATION AS PART OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THE NUA4 COMPLEX.
-!- SUBUNIT: COMPONENT OF THE NUA4 HISTONE ACETYLTRANSFERASE COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes;
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
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00:00040402; F:histone acetyltransferase activity; IDA.
GO:0016573; P:histone acetylation; IDA.
GO:0006357; P:regulation of transcription from Pol II pro.
(Rel. 39, Last sequence update) (Rel. 41, Last annotation update)
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30-MAY-2000 (Rel. 39, Last seq
28-FEB-2003 (Rel. 41, Last ann
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EAF3 OR YPR023C OR YP9367.03C
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SMBL; Z49274; CAA89277.1; -.
PIR; S54497; S54497.
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InterPro; IPR000953;
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                                                                                                                    Gaps
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                                                                               3.4%; Score 91; DB 1; Length 401; 23.0%; Pred. No. 4.7; ative 29; Mismatches 58; Indels
SMART; SM00298; CHROMO; 1.
Transcription regulation; Nuclear protein.
SEQUENCE 401 AA; 45203 MW; 63758DE9510D70DC CRC64;
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## ALIGNMENTS

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Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-brager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; leukaemia.
                     AAM39576 standard; Protein; 495 AA.
                                                                                               Human polypeptide SEQ ID NO 2721.
                                                                                                                                                                                                                                                                                                21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
09-JUL-2000; 2000US-0558042.
19-AUG-2000; 2000US-062312.
03-AUG-2000; 2000US-0653450.
14-SEP-2000; 2000US-0662191.
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                                                                     (first entry)
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                                                                                                                                                                                                        Homo sapiens.
                                                                       22-OCT-2001
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                                              AAM39576;
RESULT 1
AAM39576
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                                                                                                 The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypetides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleorides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activinibinin activity, chemcotactic/chemchietic activity, haemostatic and thrembolytic activity, cancer diagnosis and therapy, drug screening,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Note: The sequence data for this patent did not form part of the printed
                                                                Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKGMKVEVLNSDAVLPSRVYWIASVIQTAGYRVLLRYEGFENDASHDFWCNLGTVDVHPI
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                                                                                                                                                                                    Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                               Ren F, W
Zhang J;
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                                                               Qian XB,
Yang Y,
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                                                             Chen R, Ma Y, C
Xu C, Xue AJ,
t, Drmanac RT;
                                                                                                                                                                                                                                      Example 4; SEQ ID NO 2721; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                Chen R,
                                                               Asundi V, Che
Wehrman T, Xu
Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELPVSVENIKQETDD 495
29-NOV-2000; 2000US-0727344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                 2001-442253/47.
                                                               Liu C, A
Wang Z, W
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               al Similarity
495; Conserv
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                                (HYSE-) HYSEQ INC
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C.N.S disorders
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                                                             Tang YT,
Wang J, 1
Zhao QA,
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Corporation proteins (CCYPR), which are encoded by AAF59643.

COTPR and agonists of CCYPR, which are encoded by AAF59643.

COTPR and agonists of CCYPR, which are encoded by AAF59690-AAF59643.

COTPR and agonists of CCYPR are used to treat diseases or conditions associated with an encoded expression of functional CCYPR, while CCYPR antagonists are used to treat diseases or conditions associated with conversexpression of functional CCYPR. Monoclonal or plyclonal antibodies to CCYPR may be used in enzyme-linked immunosorbet associated with compounds ex, antibodies, oligomorlectides and proteins (receptors) that specifically bind to CCYPR, cCYPR itself may be used to detect compounds that modulate the activity of CCYPR. CCYPR itself may be used to generate transgenic anial models of human can be used to generate transgenic anial models of human callsease, this respect to the expression of CCYPR. CCYPR cancels and proteins with respect to the expression of CCYPR. CCYPR proteins, nucleic acide, agonists or antagonists include immune, developmental and cell signalling disorders, and cell proliferative disorders include anaemia, epilepsy, arteriosclerosis, asthma, cancer, allergies, include anaemia, epilepsy, arteriosclerosis, asthma, cancer, allergies, and be and infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human cell cycle and proliferation proteins and polynucleotides are used to treat, diagnose and prevent immune, developmental and cell signaling disorders and cell proliferative disorders including cancer
                                                                                                                                                                                                                                                                                                                                                                                 Human cell cycle and proliferation protein CCYPR-36, SEQ ID NO:36
                                                                                                                                                                                                                                                                                                                                                                                                                                Cell cycle and proliferation protein; CCYPR; human; agonist; antagonist; gene therapy; detection; gene therapy; transgenic animal disease model; immune disorder; developmental disorder, cell signalling disorder; cell proliferative disorder; cancer; tumour; anaemia; epilepsy; arteriosclerosis; asthma; allergy; diabetes mellitus; menstrual cycle disorder; bacterial infection.
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Baughn MR, Patterson C, Shah
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                                                                                                                                                                        AAB60488 standard; Protein; 495
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Lu DAM,
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99US-0153129.
99US-0164647.
481 ELPVSVENIKQETDD 495
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N-PSDB; AAF59625.
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Y, Yang J,
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Azimzai
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                                                                                                                  61 GWCAINSKILVPPRTIHAKFIDWKGYLMKRLVGSRILEPVDFHIKMVESMKYPFROGMRLE
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                                          1 MKGMKVEVLNSDAVLPSRVYWIASVIQTAGYRVLLRYEGFENDASHDFWCNLGTVDVHPI
                                                               1 MKGMKVEVLNSDAVLPSRVYWIASVIQTAGYRVLLRYEGFENDASHDFWCNLGTVDVHPI
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                Gape
               Indels
100.0%; Pred. No. 1.5e-269; ive 0; Mismatches 0;
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2000US-063450.
2000US-0662191.
2000US-0693036.
2000US-0727344.
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2000US-0598042
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               Conservative
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
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14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
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Note: The sequence data for this patent did not form part of the printed specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108 SMKYPFRQGMRLEVVDKSQVSRTRMAVVDTVIGGRLRLLYEDGDSDDDFWCHMWSPLIHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           288 TPPKGYEAQTFNWENYLEKTKSKAAPSRLFNWDCPNHGFKVGMKLEAVDLMBPRLICVAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VKRVVHRLLSIHFDGWDSEYDQWVDCESPDIYPVGWCELTGYQLQPPVAAEPATFLKAKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VKRVVHRLLSIHFDGWDSEYDQWVDCESPDIYPVGWCELTGYQLQPPVAAEPATFLKAKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATKKKKKQFGKKRKRIPPTKTRPLRQGSKKPLLEDDPQGARKISSEPVPGBIIAVRVKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATKKKKKQFGKKRKRIPPIKTRPLRQGSKKPLLEDDPQGARKISSEPVPGEIIAVRVKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         168 VGWSRRVGHGIKMSERRSDMAHHPTFRKIYCDAVPYLFKKVRAVYTEGGWFBEGMKLEAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DPLNLGNICVATVCKVLLDGYLMICVDGGPSTDGLDWFCYHASSHAIFPATFCQKWDIEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                               The invention relates to human nucleic acids (AAI57798-AAI61369) and
                                                       Wang
                                                                                                                                                                                   Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                     Ren F, W
Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                     Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.8%; Score 2436; DB 22;
99.8%; Pred. No. 6.1e-244;
live 0; Mismatches 1;
                                                   Chen R, Ma Y, (
Xu C, Xue AJ,
l, Drmanac RT;
                                                                                                                                                                                                                                           Example 2; SEQ ID NO 6293; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HLDVASPDKASSPELPVSVENIKQETDD 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HLDVASPDKASSPELPVSVENIKQETDD
                                                       Chen R,
                                                   Asundi V, Che
Wehrman T, Xu
, Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 447; Conservative
                                                                                                                           WPI; 2001-442253/47.
N-PSDB; AAI60518.
                                                   Liu C, A
Wang Z, W
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 448 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       348
                                                   ř, γ, ξ
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                                                       Tang
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RESULT 4 ABB05680

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The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB89040-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast on ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, miltiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial isonaemias; (d) wound healing; (e) indectious diseases such as viral, bacterial, fungal
                                                                                                                                                                                                                                                                                                                                                                            Cytostatic, immunosuppressive, nootropic, neuroprotective, antiviral; antiallergic, hepatotropic, antidiabetic; antiflammatory, antiulcer; vulnerary, anticonvulsant, antibacterial; antifungal; antiparasitic; cardiant; gene therapy, cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein.
511 ENYLEKTKSKAAPSRLFNMDCPNHGFKVGMKLEAVDLMEPRLICVATVKRVVHRLLSIHF 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel 1405 isolated polypeptides, useful for diagnosis, treatment and prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     claim 11; SEQ ID NO 1824; 2081pp + Sequence Listing; English.
                                                                                          571 DGWDSEYDQWVDCESPDIYPVGWCELTGYQLQPPVAA 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62.9%; Score 1688; DB 23; 99.0%; Pred. No. 2.1e-166; ive 0; Mismatches 3;
                                                 361 DGWDSEYDQWVDCESPDIYPVGWCELTGYQLQPPVAA
                                                                                                                                                                                                       ABB89448 standard; Protein; 329 AA.
                                                                                                                                                                                                                                                                                                                                         Human polypeptide SEQ ID NO 1824.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-MAY-2001; 2001WO-US16450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-MAY-2000; 2000US-205515P
                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and parasitic infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 308; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-122018/16.
N-PSDB; ABL89857.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            329 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200190304-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                 24-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Birse CE,
                                                                                                                                                                                                                                                      ABB89448;
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Best Local S
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                                                                                                                                                              RESULT 5
                                                                                                                                                                                      ABB89448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VVDKSQVSRTRMAVVDTVIGGRLRLLYEDGDSDDDFWCHMWSPLIHPVGWSRRVGHGIKM 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CKVLLDGYLMICVDGGPSTDGLDWFCYHASSHAIFPATFCQKNDIELTPPKGYEAQTFNW 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENYLEKTKSKAAPSRLFNMDCPNHGFKVGMKLEAVDLMEPRLICVATVKRVVHRLLSIHF 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VVDKSQVSRTRMAVVDTVIGGRLRLLYEDGDSDDDFWCHMWSPLIHPVGWSRRVGHGIKM 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes assemblages and computer readable media comprising novel human cDNA sequences and clones derived from human foetal brain, foetal kidney, melanoma, testis and amygdala cDNA libraries. ABA33702 to ABA33766 represent human cDNA sequences from the present invention which encode the proteins given in ABB0562 to ABB05729. The human cDNA sequences and clones can be used in gene therapy. The clones may be used in a variety of applications, for example they may be used in profiling assays, for providing large arrays of human genetic material for implementing large-scale screening strategies and for treating diseases via gene therapy procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               211 MKGMKVEVLNSDAVLPSRVYWIASVIQTAGYRVLLRYEGFENDASHDFWCNLGTVDVHPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GWCAINSKILVPPRTIHAKFTDWKGYLMKRLVGSRTLPVDFHIKMVESMKYPFRQGMRLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SERRSDMAHHPTFRKIYCDAVPYLFKKVRAVYTEGGWFEEGMKLEAIDPLNLGNICVATV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CKVLLDGYLMICVDGGPSTDGLDWFCYHASSHAIFPATFCQKNDIELTPPKGYEAQTFNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKGMKVEVLNSDAVLPSRVYWIASVIQTAGYRVLLRYEGFENDASHDFWCNLGTVDVHPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cDNA sequences and clones derived from human fetal brain, kidney, melanoma, testis and amygdala cDNA libraries, useful in screening and therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                    foetal kidney; melanoma; testis; amygdala;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 2185; DB 23;
Pred. No. 1.2e-217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
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100.0%; Pred. No. 1...
... 0; Mismatches
                                                                                                                                              Human transmembrane protein clone amy2_li14.
                                                                                                                                                                                                         gene therapy; chromosome 22q13.31-13.33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GEHU-) GERMAN HUMAN GENOME PROJECT.
           ABB05680 standard; Protein; 617 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1, Page 130; 611pp; English.
                                                                                                                                                                                                                                                                                                                                                                                           25-APR-2001; 2001WO-IB02050
                                                                                                                                                                                                                                                                                                                                                                                                                                     25-APR-2000; 2000US-199380P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100. es 397; Conservative
                                                                                                                                                                                      foetal brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-055860/07.
N-PSDB; ABA93718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            617 AA;
                                                                                                                                                                                                                                                                                                   WO200198454-A2.
                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                              27-DEC-2001
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                                                      ABB05680
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1 MKGMKVEVLNSDAVLPSRVYWIASVIQTAGYRVLLRYEGFENDASHDFWCNLGTVDVHPI

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241 CKVILIDGYLMICVDGGPSTDGLDWFCYHASSHAIFPATFCQKNDIELIPPRGYEAQTFNW<sup>*</sup>300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DGWEERYDOWYDCESPDLNPVGWCQLTGYQLQPPASQSSRESQSASSKQXKKAKSQQYKG
                                                                                                                                                                                                                                                                                                                                                                                                    2 KGMKVEVLNSDAVLPSRVYWIASVIQTAGYRVLLRYEGFENDASHDFWCNLGTVDVHPIG
                                                                                                                                                                                                                                                                                                                                                                                                                          SERRSDMAHHPTFRKIYCDAVPYLFKKVRAVYTEGGWFEEGMKLEAIDPLNLGNICVATV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DGWDSEYDQWYDCESPDIYPVGWCELTGYQLQPPVAAEPATPLKAKEATKKK-KKQFGKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WCAINSKILVPPRIIHAKFIDWKGYLMKRLVGSRTLPVDFHIKMVESMKYPFRQGMRLEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VDKSQVSRTRMAVVDTVIGGRIRLLYBDG-DSDDDFWCHMWSPLIHPVGWSRRVGHGIKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDITKKODGH-----PDTPPHLFAKVKEVDQSGEWFKEGMKLEAIDPLNLSTICVATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 ENYLEKTKSKAAPSRLFNMDCPNHGFKVGMKLEAVDLMEPRLICVATVKRVVHRLLSIHF
transcription factors, splicing factors, capping factors, transport proteins, translation factors or replication factors that modulate HSC activity, especially differentiation or replication. The invention provides claimed methods: for identifying PHSC-specific nucleic acids; for generating a stem cell/progenitor cell from PHSCs; for identifying the presence of a PHSC in a sample; for identifying the presence of a PHSC in a sample; for identifying the presence in a sample of a compound that modulates HSC activity; for using such a compound to treat an immune system acondition, especially leukaemia; for introducing exogenous nucleic acid into a HSC; and for ex vivo expansion of HSCs. Also claimed are vectors, host cells, and an antibody that specifically binds a
                                                                                                                                                                                                                                                                                                                Length 631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RKRIPPIKTRPLRQGSKKPLLEDDPQGARKISSEPVPGELIAVRVKEE 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |:: :: |: |: |: |: | HICATISOL-----KEELLDGEDYSFLHGASDQESNGSATVYIKQE 630
                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, angiogenesis-associated transcript, angiogenesis; angiogenesis-associated disease; cancer; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Angiogenesis-associated human protein sequence #102
                                                                                                                                                                                                                                                                                                             52.6%; Score 1410; DB 21;
56.2%; Pred. No. 4.6e-137;
iive 67; Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 56.2<sup>†</sup>
Matches 263; Conservative
                                                                                                                                                                                                                                  an HSC-specific protein.
                                                                                                                                                                                                                                                                              631 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-OCT-2002
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                                                                                                                                                                                                                                                                              Sequence
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ID ABU0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is that of a mouse haematopoietic stem cell (HSC) specific protein. It is an example of claimed HSC-specific proteins (see AAY79176-93) predicted from novel isolated HSC-specific nucleic acids (see AAY79131). The HSCs are especially primitive HSCs (PHSCs) such as umbilical cord cells, bone marrow cells and foetal liver cells. The encoded proteins are growth factors,
  61 GWCAINSKILVPPRTIHAKFTDWKGYLMKRLVGSRTLPVDFHIKMVESMKYPFRQGMRLE
                                                                                                                                                                                                                                                                        181 SERRXDMAHHPTFRKIYCDAVPYLFKKVRAVYTEGGWFEEGMXLEAIDPINLGNICVATV
                                                                                                                                                    121 VVDKSQVSRTRMAVVDTVIGGRLRLLYEDGDSDDDFWCHMWSPLIHPVGWSRRVGHGIKM
                                                                                                                                                                                 121 VVDKSQVSRTRMAVVDTVIGGRLRLLYEDGDSDDDFWCHMWSPLIHPVGWSRRVGHGIRM
                                                                                                                                                                                                                                                                                                                      CKVLLDGYLMICVDGGPSTDGLDWFCYHASSHAIFPATFCQKNDIELTPPKGYEAQTFNW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      daematopoietic stem cell; immune system disorder; leukaemia; antileukaemic; immunomodulator; therapy; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haematopoietic stem cell specific protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "encoded by TAT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 21; Page 229-231; 256pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY79183 standard; Protein; 631 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note= "encoded
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                                                                                                                                                                                                                                                                                                                                                                                                         ENYLEKTKSKA 311
                                                                                                                                                                                                                                                                                                                                                                                                                                              ENYLEKTKSKA 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYPR-) UNIV PRINCETON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lemischka I, Moore K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-237650/20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
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16; Gaps

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ABB78695 standard; Protein; 410
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                                                                                                                               Caenorhabditis
                                                                                                                                                                        Homo sapiens.
                                                                            17-JUL-2002
                                                                                                                                                                                                                        13-DEC-2001
                                                    ABB78695;
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ABB78695
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                                                                                                                                                                                                                                                                     The present invention relates to methods and compositions for detecting an angiogenesis-associated transcript in a cell in a patient. The method involves contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence at least 80% identical to any of the angiogenesis-associated human polynucleotide sequences given in the specification. These angiogenesis-associated polynucleotide sequences comprise genes that exhibit changes in expression levels as a function of time in tissue cubargoing angiogenesis. The method and the polynucleotide sequences of the invention are useful for diagnosing and treating angiogenesis and angiogenesis-associated diseases e.g. cancer. The polynucleotide sequences are also useful in the gene therapy of such disorders. The angiogenesis-associated proteins encoded by the polynucleotide sequences are useful in as a vaccine for therapeutic and prophylactic immunisation. Abu03456-ABU03569 represent angiogenesis-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 WCAASGKPLVPPRTIQHKYTNWKAFLVKRLTGAKTLPPDFSQKVSESMQYPFKPCMRVEV 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 VDKSQVSRTRMAVVDTVIGGRLRLLYEDG-DSDDDFWCHMWSPLIHPVGWSRRVGHGIKM 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SERRSDMAHHPTFRKIYCDAVPYLFKKVRAVYTEGGWFEEGMKLEAIDPLNLGNICVATV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SDITKKQDGH------FDTPPHLFAKVKEVDQSGEWFKEGMKLEAIDPLNLSTICVATI 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243 RKVLADGFLMIGIDGSEAADGSDWFCYHATSPSIFPVGFCEINMIELTPPRGYTKLPFKW 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENYLEKTKSKAAPSRLFNMDCPNHGFKVGMKLEAVDLMEPRLICVATVKRVVHRLLSIHF 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 ENVRVEVENTDCSLPTKVFWIAGIVKLAGYNALLRYEGFENDSGLDFWCNICGSDIHPVG 69
                                                                                                                                                                                Detecting angiogenesis-associated transcript in a cell for diagnosing and treating cancer by contacting a sample with a polynucleotide that exhibits changes in expression level as a function of time in tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VDKRHLCRTRVAVVESVIGGRLRLVYEESEDRTDDFWCHMHSPLIHHIGWSRSIGHRPKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 KGMKVEVLNSDAVLPSRVYWIASVIQTAGYRVLLRYEGFENDASHDFWCNLGTVDVHPIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WCAINSKILVPPRTIHAKFTDWKGYLMKRLVGSRTLPVDFHIKMVESMKYPFRQGMRLEV
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60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.0%; Score 1395; DB 24; Length 410; 62.9%; Pred. No. 8.5e-136; Live 55; Mismatches 84; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DGWDSEYDQWVDCESPDIYPVGWCELTGYQLQPPVA 396
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                                                                                                                                                                                                                                              Example 2; Page 275; 291pp; English.
                                                                                                                   Watson SR,
                                                                                        (EOSB-) EOS BIOTECHNOLOGY INC
             2001US-0791390.
2001US-285475P.
2001US-310025P.
2001US-350666P.
                                                               29-NOV-2001; 2001US-334244P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                        undergoing angiogenesis
                                                                                                                   Glynne R,
                                                                                                                                            WPI; 2003-040681/03.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   410 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein sequences
                                                                                                                                                        N-PSDB; ABX08841
                                     03-AUG-2001;
                                                  13-NOV-2001;
                          19-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249;
                                                                                                                   Murray R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130
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The present invention describes a substantially pure nematode C. elegans (Caenorhabditis elegans) nucleic acid (I) encoding a LIN-8 polypeptide (see ABB78649), or LIN-6 polypeptide (see ABB78649), or LIN-6 polypeptide (see ABB78649), or LIN-6 polypeptide (see ABB78650), where the polypeptides comprise at least 130, 110, 130 contiguous amino acids of the 386, 322 and 498 amino acid sequences given in ABB78649 to ABB78650, and modulate cell proliferation. (I) has modulating proliferation of a cell, and for identifying the compound that modulates cell proliferation. (I) is useful for modulates cell proliferation. (I) can be used for identifying the compound that modulates cell proliferation disease, or an increased chance of developing the disease, by measuring lin-8, Lin-56 or Lin-61 proliferation disease, or an increased chance of developing the disease, by measuring lin-8, Lin-56 or Lin-61 polypeptide in the sample using Ab or measuring amount of lin-8, lin-56, lin-61 mRNA in the sample. (I) is also useful for identifying the compound that modulates cell proliferative diseases including cancer, as well as in diagnosing and treating cell proliferative diseases. (I) is also useful for identifying the compound that modulates conducting cell proliferative diseases uch as mammals and may be used to identify therapeutic compounds. The present sequence represents a human hyp (heat shock procein) protein which is given in comparison with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Caenorhabditis elegans nucleic acid involved in tumor suppressor pathway, encoding LIN-8, LIN-56 or LIN-61 polypeptide, useful for diagnosing and treating cell proliferative diseases such as cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8;
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62.6%; Pred. No. 5.7e-135;
ive 56; Mismatches 84;
Human hap BAA90919 protein sequence SEQ ID NO:68
                                                                                                                                   cell proliferation; nematode; cancer; mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MASI ) MASSACHUSETTS INST TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Fig 8; 116pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lu X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-JUN-2000; 2000US-208802P
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248; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Horvitz HR, Davison EM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-401590/43.
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189
                                                                                                                      SERRSDMAHHPTFRKIYCDAVPYLFKKVRAVYTEGGWFEEGMKLEAIDPLNLGNICVATV 240
                                                                                                                                                                                                                                          CKVLLDGYLMICVDGGPSTDGLDWFCYHASSHAIFPATFCQKNDIELIPPKGYEAQTFNW 300
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13
VDKSQVSRTRMAVVDTVIGGRLRLLYEDG-DSDDDFWCHMWSPLIHPVGWSRRVGHGIKM 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophilar. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA
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                                   Drosophila; developmental biology; cell signalling; insecticide;
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Length 891;

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Query Match

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                          Indels
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            Pred. No. 9.4e-106;
5; Mismatches 162;
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43.48; PIC. 75;
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            Best Local Similarity
Matches 234; Conserv
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rebroprotective; cytostatic; rheumatic; gene therapy;
                                                                                                                               The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and insectiodes. Therefore in higher eukaryotes for the development of insectiodes, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL016176-ABL05611), expressed DNA sequences (ABL01840-ABL06115) and the encoded proteins
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                     ID NO 27069; 21pp + Sequence Listing; English
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neuroprotective; antiparkinsonian; protein therapy; BST;
expressed sequence tag.
                                                                                                                                                                                                  41.4%; Score 1111; DB 22;
43.4%; Pred. No. 1.6e-105;
iive 75; Mismatches 162;
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                     Disclosure; SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides the protein and coding sequences of 444 novel human proteins. These were isolated from expressed sequences tags (ESTB). They can be used to stimulate cell growth, to regulate haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth e.g. in burn treatment, to regulate the immune system e.g. to treat multiple sclerosis, to regulate hemostasis or thrombolysis e.g. to treat stroke and cancer, to screen for drugs, to treat inflammatory conditions of the inmutities, and to treat nervous system disorders e.g. parkinson's disease. The present sequence is a protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        228 ELQPPSAIRHLKNEAEWQEILAKVKEEEEPLPSYLFKDKQVIGIHT----FSVMMKLEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             177 GIKMSERRSDMAHHPTFRKIYC-----DAVP-YLF--KKVRAVYTEGGWFEEGMKLEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      286 ELTPPKGYEAQTFNWENYLEKTKSKAAPSRLFNMDCPNHGFKVGMKLEAVDLMEPRLICV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GMKVEV-LNSDAVLPSRVYWIASVIQTAGYRVLLRYEGFENDASHDFWCNLGTVDVHPIG
                                                                                                                                                                                                                                                                                                                                                                                                                    An isolated polynucleotide for treating diseases associated with its encoded polypeptide such as cancer and multiple sclerosis -
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                                                                                                                                                                                                                                                                                Ren
                                                                                                                                                                                                                                                                             QA,
                                                                                                                                                                                                                                                                             Zhao
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23.1%; Score 620.5; DB 23; 31.9%; Pred. No. 8.6e-55; iive 91; Mismatches 205;
                                                                                                                                                                                                                                                                             Zhang J,
RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 20; SEQ ID NO 762; 509pp; English.
                                                                                                                                                                                                                                                                                                 Drmanac
                                                                                                                                                                                                                                                                                Asundi
                                                                                                                                                                                                                                                                             Zhou P, As
Wehrman T,
                                                                                                                                    10-SEP-2001; 2001WO-US26015
                                                                                                                                                                                 11-SEP-2000; 2000US-0659671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              161; Conservative
                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-292408/33.
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                                                                                                                                                                                                                                                                             Liu C,
Yang Y,
                                                                                                                                                                                                                                (HYSE-) HYSEQ INC
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                                          WO200222660-A2
Homo sapiens.
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The invention relates to an isolated polynucleotide (I) comprising a nucleotide sequence selected from any of 948 sequences (ABZ11119-ABZ12066) or their mature protein coding portion, active domain coding protein or complementary sequences. The polynucleotides are useful for identifying expressed genes or for physical mapping of human genome. The encoded polypeptides (ABP68902-ABP68949) are useful as molecular weight markers, as a food supplement, for generating antibodies, in medical imaging, screening and diagnostic assays and for treating cell-proliferative disorders (cancer), neurodegenerative disorders (cancer), neurodegenerative disorders (scancer), neurodegenerative disorders scales), autoimmune diseases (multiple sclerosis, diabetes, lupus) genetic disorders, myeloid or lymphoid disorders, platelet or coagulation disorders, wound, burns, incision, ulcers, liver or lung fibrosis, infections (bacterial, viral, fungal, parasitic), arthritis, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cell-proliferative disorder; neurodegenerative disease; bacterial; Parkinson's disease; Alzheimer's disease; autoimmune disease; Alzheimer's disease; autoimmune disease; autiliple sclerosis; disbetes; genetic disorder; wound; burn; infection; arthritis; cytostatic; immunomodulator; noctropic; neuroprotective; antiparkinsonian; antidiabetic; immunosuppressive; dermatological; haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoacide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ren F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genome mapping; gene therapy; food supplement; virus; fungus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotides comprising sequences assembled from expressed agequence tags (ESTS), useful for treating cell-proliferative, neurodegenerative, autonimmune, genetic, myeloid or lymphoid, or platelet or coagulation disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhang J, Zhao QA, ]
, Wang Z, Ghosh M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goodrich RW, Asundi V, Zha
na Y, Yamazaki V, Chen R,
Wang D, Drmanac RT;
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465 KEEHLDVASP--DKASSPELPVSV 486
                                                506 YFNHRCFSGPYLNKGRIABLPQCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human polypeptide SEQ ID NO 1614.
                                                                                                                                                                                                                                            ABP69567 standard; Protein; 894
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J. Wang D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35-MAR-2002; 2002WO-US05095
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T, Wang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-759812/82
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Wehrman T,
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215 GGWFEEGMKLEAIDPLNLGNICVATVCKVLLDGYLMICVDG-GPSTDGLDWFCYHASSHA 273
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                                                                                                                                                                                    246 CQE-----NKYRMDPPSEIYPLKMASEWKCTLEKSLIDAAKFPLPMEVFKDHADLRSH 298
                                                                                                                                                                                                                                                                                           ILPVQWCLKNGVSLTPPKGYSGQDFDWADYHKQHGAQEAPPFCFRNTSFSRGFTKNMKLE 415
                                                                                                                                                                                                                                                                                                                       334 AVDLMEPRLICVATVKRVVHRLLSIHFDGWDSEYDQ-WVDCESPDIYPVGWCELTGYQLQ 392
62
                                                                                                                                                           --MAHH--PIFRKIYCDAVPY----LFKKVRAVYTE
                                                                                                                       IFPATFCQKNDIELTPPKGYEAQTFNWENYLEKTKSKAAPSRLFNMDCPNHGFKVGMKLE
                                                                                                       115 -QGMRLEVVDKSQVSRTRMAVVDTVIGGRLRLLY---EDGDSDDDFWCHMMSPLIHPVGW
GMKVEVLNSDAVLPSRVYWIASVIQTAGYRVLLRYEGFENDASHDFWCNLGTVDVHPIGW
                                                   CAINSKILVPPRTIHAKFTDWKGYLMKRLVGSRTLPVDFHIKMVESMKYPFR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to isolated polynucleotide (I)
                                                                                                                                                                                                                                                                                                                                                                          393 PPVAAEPATPLKAKEAT---KKKKKQFGKKRRIPPT 426
                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; SEQ ID No 44757; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human diagnostic protein #14389.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABG14398 standard; Protein; 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAR-2000; 2000US-0540217, 23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                          171 SRRVGHGIKMSERRSD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-639362/73.
N-PSDB; AAS78585.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC
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Gaps

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Indels

Length 894;

22.8%; Score 611; DB 23; 34.1%; Pred. No. 8.8e-54; Live 65; Mismatches 170;

Conservative

Query Match Best Local Similarity Matches 156; Conserv

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polymerase chain reaction (PCR) Primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymuleorides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful in generating antibodies against it, defecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating in medical in polypeptide and polymoleculae sequences have applications in disorders involving aberrant protein expression or biological activity. The polypeptide and polymolecules sequences have applications in dispnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human dispnostic amino acid sequences of the invention.

Oute: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the wipo int/pub/published_pot_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IHAKFIDWKGYLMKRLVGSRTLPVDFHIKMVESMKYPFRQGMRLEVVDKSQVSRTRMAVV 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DIVIGGRIRLIYEDG-DSDDDFWCHMWSPLIHPVGWSRRVGHGIKMSERRSDMAHHPTFR 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anti-inflammatory; immunosuppressive; osteopathic; cytostatic; anti-HIV; haemostatic; nephrotropic; antianaemic; antipsoriatic; hepatotropic; gene therapy; protein replacement therapy; cell proliferative disorder; cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myaloma; sarcoma; anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 PSRV----ALEQECGYNALLRYEGFENDSGLDFWCNICGSDIHPVGWCAASGKPLVPPRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSRVYWIASVIQTAGYRVLLRYEGFENDASHDFWCNLGTVDVHPIGWCAINSKILVPPRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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(II) sequences. (I) is useful as hybridisation probes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21.9%; Score 587; DB 22;
56.1%; Pred. No. 2.8e-52;
tive 28; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABU11746 standard; Protein; 538 AA
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29-MAR-2001; 2001US-280067P.
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Matches 111; Conservative
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This invention describes a novel disease detection and treatment molecule polypeptide (MDDT) which has anti-inflammatory, immunosuppressive, osteopothic, cytostatic, anti-HIV, haemostatic, nephrotropic, contemporatic, anti-HIV, haemostatic, nephrotropic, antianaemic, artiposoriatic and heparotropic activity. The polymucleotides and the polypeptides of the invention can be used for gene therapy, protein replacement therapy and are useful for treating a variety of diseases or conditions. These polypeptides or polymucleotides are particularly useful for diagnosing treating or preventing cell particularly useful for diagnosing treating or preventing cell printing in the disconse, including adenocarcinoma, lumphoma, melanoma, myeloma or sarcoma), anaemia, Crohn's disease, acquired immunodeficiency syndrome (AIDS), Goodpasture's syndromes, inflammation, setcoporosis, thrombocytopaenia, psoriasis or hepatitis. ABUI1450-ABUI1445 represent the MDDT polymucleotides encoded by ABUI1450-ABUI1845 represent the MDDT polymucleotides encoded by ABUI1450-ABUI1845 represent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but was obtained in electronic format from WIPO at
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JL, Yu JY, Tuason O, Yap PE, Amshey SR;
C, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;
H, Lewis SA, Chen AJ, Panzer SR, Harris B;
Lo A, Lan RY, Urashka ME;
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             16-MAY-2001; 2001US-291280P.

17-MAY-2001; 2001US-291829P.

17-MAY-2001; 2001US-291849P.

20-UNN-2001; 2001US-299428P.

20-UNN-2001; 2001US-299776P.
                                                                                                                                                                   (INCY-) INCYTE GENOMICS INC.
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Hillman JL,
                                                                                                                                                                                                                                             Daugherty SC, Dam TC,
Peralta CH, David MH,
Flores V, Marwaha R,
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N-PSDB; ABX34736.
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                             -----PTKTRPLRQGSKKPLLEDDPQGA
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iE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
Y, SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin E,
Y, David MH, Leas SA, Chen AJ, Panzer SR, Harris B;
', Marwaha R, Lo A, Lan RY, Urashka ME;
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HFDGWDSEYDQWVDCESPDIYPVGWCELTGYQLQPPVA-AEPAT----
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2001US-280067P.
2001US-280068P.
2001US-291809P.
2001US-291829P.
2001US-291849P.
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N-PSDB; ABX34823.
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Daugherty SC,
Peralta CH, Da
Flores V, Marw
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19-JUN-2001;
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This invention describes a novel disease detection and treatment molecule bylypetide (MDT) which has anti-inflammatory, immunosupressive, osteopethic, cytostatic, anti-inflammatory, nephrotropic, antipaoriatic and hepatotropic activity. The polynucleotides

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protein replacement therapy and are useful for treating a variety of diseases or conditions. These polypeptides or polymucleotides are particularly useful for diagnosing, treating or preventing cell particularly useful for diagnosing, treating or preventing cell profilerative disorders (e.g. cancers including adenocarcinoma, cell-ukaemia, lymphoma, melanoma, myeloma or sarcoma), anaemia, CC disease, acquired immunodeficiency syndrome (AIDS), Goodpasture's syndromes, inflammation, osteoporosis, thrombocycopenia, psoriasis or syndromes, inflammation, osteoporosis, thrombocycopenia, psoriasis or by ABU11450-ABU11845 represent the MDDT polymucleotides encoded by ABU11450-ABU11845, described in the disclosure of the invention.

C NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed of th
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Derugence 6, Application US/08652153

Sequence 6, Application US/08652153

Parent No. 2514266

SENTERT NOTATION: Mammalian Sex Comb on Midleg Acts as a Tumor Suppressor NUMBER OF REGURNES: 8

CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
COMPUTER: 4560 Horton Street

STATE: California
CONPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatibl
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S-08-852-153-4
Sequence 4, Application US/08852153
Sequence 4, Application US/08852153
Sequence 4, Application US/08852153
Septent No. 5914266
GENERAL INFORMATION:
APPLICANT: Randazzo, Filippo
ATTILE OF INVENTION: Mammalian Sex Comb on Midleg Acts as a Tumor Suppressor NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----KQFGKKRKIP------PT 426
216 PPGTKVVIPKNPYPASDVNTEKPSIHSSTKTVLEHQPGQRGRKPGKKRGRTPKTLISHPI 275
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                                             425 --PTKT-RPL-----RQGSK-KPLLEDDPQGARKISSEPVP 456
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.2%; Score 353.5; DB 2; 36.1%; Pred. No. 1.1e-30; tive 30; Mismatches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     395 VAAEPATPLKAKEATKKKK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPERINCE DOCKET WINBER: 122.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 923-3888
TELEPAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
ANAME: GUCH, JOSEPH H.
REGISTRATION NUMBER: 31,26
REGISTRATION NUMBER: 31,26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 101; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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Best Local &
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APPLICANT: Randazzo, Filippo
TITLE OF INVENTION: Mammalian Sex Comb on Midleg Acts as a Tumor Suppressor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
                                                                          ---KQFGKKRKRIP----- 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       278 TFCQKNDIELTPPKGYEAQTFNWENYLEKTKSKA--APSRLFNMD--CPNHG-FKVGMKL 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BAVDLMEPRLICVATVKRVWHRLLSIHFDGWDSEYDQWVDCESPDIYFVGWCELTGYQLQ 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 BAVDRKNPHFICPATIGEVRGSEVLVTFDGWRGAFDYWCRFDSRDIFPVGWCSLTGDNLQ 215
    67 GNCEKNGGMLQPPLGFRLNASSWPMFLLKTLNGAEMAPIRIFHKEPPSFSHNFFKMGMKL 126
                                                                                                                                                                                  187 PPGTKVVIPKNPYPASDVNTEKPSIHSSTKTVLEHQPGQRGRKPGKKRGRTPKTLISHPI 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              218 FEEGMKLEAIDPLNLGNICVATVCKVLLDGYLMICVDGGPSTDGLDWFCYHASSHAIFPA 277
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                                                BAVDLMEPRLICVATVKRVVHRLLSIHFDGWDSEYDQWVDCESPDIYPVGWCELTGYQLQ
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                                                                                                                                                                                                                                                                           247 SAPSKTAEPLKFPKKRGPKPGSKRKPRTLLNPPPASPTTSTPEP 290
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARS: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 357.5; DB 2;
; Pred. No. 4.5e-31;
31; Mismatches 102;
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                                                                                                                                         393 PP--VAAEPATPLKAKEATKKKK--
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Patent No. 5914266
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ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 31,261
REPERSICE/DOCKET NUMBER: 122.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 923-3888
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35.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (510) 655.3542
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 35.94
Matches 102; Conservative
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CITY: Emeryville
STATE: California
COUNTRY: U.S.A.
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...O, YURI
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CTSUKA, KAORU
...LAMT: TREE, KYOTAGO
...LICANT: TAMECHIKA, ICHIRO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NACHIKO
APPLICANT: NACHARA, TSUTCMU
APPLICANT: NACHARA, TSUTCMU
APPLICANT: NACHARI, KENJI
APPLICANT: NACHARI, TOUGO-03-12
BRIOR FILING DATE: 2002-03-14
NUMBER OF SEQ ID NOS: 3381
SEQ ID NO 2556
TYPE: PRIOR PRIOR PRODE
CURRANISM: HOMO PT
COSSANISM:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 56, Appl
Sequence 68, Appl
Sequence 312, Appl
Sequence 71, Appli
Sequence 72, Appli
Sequence 72, Appl
Sequence 28826, A
Sequence 38836, A
Sequence 38836, A
Sequence 3262, Appl
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Sequence 4101, Ap
Sequence 1824, Ap
                                                                                                                                                                                                                        February 4, 2004, 09:08:22 ; Search time 39 Seconds (without alignments) 2657.544 Million cell updates/sec
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2683
1 MKGMKVEVLNSDAVLPSRVY......KASSPELPVSVENIKQETDD 495
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCCMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_MBW PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_NEW PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCCMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US06_PUBCCMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US08_NEW PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCCMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCCMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCCMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCCMB.pep:*
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13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCCMB.pep:*
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19: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCCMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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2 US-10-108-260A-4101
US-10-260A-4101
US-10-1824
0 US-09-789-919-56
0 US-10-108-68
0 US-10-10-04-04-3512
0 US-09-872-523-5
0 US-09-872-523-5
0 US-09-872-523-7
0 US-09-872-523-7
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0 US-09-872-523-7
0 US-10-029-386-27484
US-09-864-761-38826
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Match Length
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Perfect score:
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No.
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Sequence 12, Appl Sequence 7, Appli Sequence 7, Appli Sequence 93, Appl Sequence 10, Appl Sequence 10, Appl Sequence 1159, Appl Sequence 12, Appl Sequence 12, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 13, Appl Sequence 13, Appl Sequence 13, Appl Sequence 38662, A Sequence 38662, A Sequence 38662, A Sequence 38662, A Sequence 38663, Appl Sequence 38663, Appl Sequence 3863, Appl Sequence 5, Appli Sequence 5, Appli	ednence ednence
09-801-574-1 10-204-872-523- 10-204-872-523- 10-204-872-523- 10-204-872-523- 10-204-872-523- 10-204-872-523- 10-204-872-523- 10-204-872-523- 10-204-872-523- 10-204-872-523- 10-204-872-523- 10-204-872-523- 10-204-872-523- 10-204-872-523- 10-304-872-523- 10-304-872-523- 10-304-872-523- 10-304-872-523- 10-304-872-873- 10-304-872-873- 10-304-873-873-873-873-873-873-873-873-873-873	10-354-951 10-354-951 10-008-566 10-078-059
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#### AL I GNMENTS

Sequence 2556, Application US/10094749 Publication No. US20030219741A1 GENERAL INFORMATION:

US-10-094-749-2556

APPLICANT: ISOGAL, TAKAO
APPLICANT: SUGITAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: SATO, HIROYUKI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZKKO
APPLICANT: ISHII, SHIZKKO
APPLICANT: ISONO, YUUKO
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YUKI

US-10-029-386-30438 US-10-104-047-2262 US-10-104-047-3204 US-10-264-049-2539

398 389.5 373.5

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241 CKVLLDGYLMICVDGGPSTDGLDWFCYHASSHAIFPATFCQKNDIELTPPKGYEAQTFNW 300
240 VVDKSQVSRTRMAVVDTVIGGRLRLLYEDGDSDDDFWCHMWSPLIHPVGWSRRVGHGIRM
                                                                                                                                                                                                                                    361 DGWDSEYDQWVDCESPDIYPVGWCELTGYQLQPPVAA 397
                                                                                                                                                                                                                                                           DGWDSEYDQWVDCESPDIYPVGWCELTGYQLQPPVAA 516
                                                                                                                                                                                                                                                                                                                                             ; Sequence 1824, Application US/10264237; Publication No. US20040009491A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 99.0
Matches 308; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                 RESULT 3
US-10-264-237-1824
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                   Length 705;
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GENERAL INFORMATION:
TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA; FILE REFERENCE: H1-A0106; CURRENT APPLICATION NUMBER: US/10/108,260A; CURRENT FILING DATE: 2002-03-27; NUMBER OF SEQ ID NOS: 5458; SOFTWARE: PatentIn Ver. 2.1; SEQ ID NO 4101
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8.9e-210;
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                  Score 2679; DB 12;
Pred. No. 4.5e-259;
0; Mismatches 1;
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100.0%; Pred. No. 8.9
ive 0; Mismatches
                99.9%;
nilarity 99.8%;
Conservative 0
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Matches 397; Conservative
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ORGANISM: Homo sapiens
                                  Similarity
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US-10-108-260A-4101
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                  Query Match
Best Local S:
Matches 494
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NAME/KEY: MISC FEATURE LOCATION: (185)
CTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids FRATURE:
NAME/KEY: MISC FEATURE
LOCATION: (223)
CTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-237-1824 359 300 420 ENYLEKTKSKAAPSRLFNMDCPNHGFKVGMKLBAVDLMEPRLICVATVKRVVHRLLSIHF 479 120 61 GWCAINSKILVPPRITIHAKFTDWKGYLMKRLVGSRTLPVDFHIKMVESMKYPFRQGMRLE 120 180 240 360 CKVLLDGYLMICVDGGPSTDGLDWFCYHASSHAIFPATFCQKNDIELTPPKGYEAQTFNW 419 ENYLEKTKSKAAPSRLFNMDCPNHGFKVGMKLEAVDLMEPRLICVATVKRVVHRLLSIHP 360 VVDKSQVSRTRMAVVDTVIGGRLRLLYEDGDSDDFWCHMWSPLIHPVGWSRRVGHGIKM 180 9 9 300 SERRSDMAHHPTFRKIYCDAVPYLFKKVRAVYTEGGWFEEGMKLEAIDPLNLGNICVATV 181 SERKSTMAHHPTERKIYCDAVPYLFKKVRAVYTEGGWFEEGWKLBAIDPLNIGNICVATV 181 SERRYDMAHHPTERKIYCDAVPYLFKKVRAVYTEGGWFEEGHXLFAIDPLNIGNICVATV 241 CKVLLDGYLMICVDGGPSTDGLDWFCYHASSHAIFPATFCQKNDIELTPPKGYEAQTFNW CKVLLDGYLMICVDGGPSTDGLDWFCYHASSHAIFPATFCQKNDIELTPPKGYEAQTFNW 1 MKGMKVEVLNSDAVLPSRVYWIASVIQTAGYRVLLRYEGFENDASHDFWCWWGTVDVHPI SERRSDMAHHPTFRKIYCDAVPYLFKKVRAVYTEGGWFEEGMKLEAIDPLNLGNICVATV 61 GWCAINSKILVPPRIIHAKFIDWKGYLMKRLVGSRILPVDFHIKMVESMKYPFRQGMRLE VDVHPI 1 MKGMKVEVLNSDAVLPSRVYWIASVIQTAGYRVLLRYEGFENDASHDFWQNLG APPLICANT: Birse et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERENCE: PAL31P1
CURRENT APPLICATION NUMBER: US/10/264,237
CURRENT FILING DATE: 2002-10-04
FRIOR PAPLICATION NUMBER: PCT/US01/16450
PRIOR PILING DATE: 2001-05-18
PRIOR PILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: US 60/205,515
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 2876
SOFTMARE: PATENTIN Ver. 3.1
SEQ ID NO 1824 62.9%; Score 1688; DB 12; Length 329; 99.0%; Pred. No. 2.8e-160; iive 0; Mismatches 3; Indels 0

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CURRENT APPLICATION NUMBER: US/09/872,523
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Matches 248; Conservative
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; ORGANISM: Homo sapiens
US-10-104-047-3512
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Best Local Similarity
Matches 121; Conserv
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                                                                                                                            Sequence 56, Application US/09789919

Sequence 56, Application US/09789919

GENERAL INFORMATION:
APPLICANT: Lemischka, Ihor
APPLICANT: Moore, Kareri
ATILE OF INVENTION: GENLS THAT REGULATE HEMATOPIETIC BLOOD FORMING STEM
TITLE OF INVENTION: CELLS AND USES THEREOF
FILE REFERENCE: 2275-1-005
CURRENT APPLICATION NUMBER: US/09/789,919
CURRENT FILING DATE: 2001-02-21
NUMBER OF SEQ ID NOS: 96
SOFTWARE PARENT NOS: 96
SOFTWARE PARENT NOS: 96
LENGTH: 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         410 RKVLADGFLMIGIDGSEAADGSDWFCYHATSPSIFPVGFCEINMIELTPPRGYTKLPFKW
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APPLICANT: Davison, Eva M.
APPLICANT: Du, Xiaowei
TITLE OF INVENTION: A Tumor Suppressor Pathway in C. Elegans
FILE REFERENCE: 01997/536002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           52.6%; Score 1410; DB 9; 56.2%; Pred. No. 5.1e-132;
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Patent No. US20020137906A1
GENERAL INFORMATION:
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Best Local Similarity 56.2%
Matches 263, Conservative
            ENYLEKTKSKA 311
                                           301 ENYLEKTKSKA 311
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70 W.CAASGKPLVPPRTIQHKYTNWKAFLVKRLTGAKTLPPDFSQKVSESMQYPFKFCMRVEV 129
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Publication No. US20030236392A1

GENERAL INCOMATION:

APPLICANT: HELIX RESEARCH INSTITUTE

TILLE OF INVENTION: No. US20030236392A1e1 full length cDNA

FILE REFREENCE: H1-A0105

CURRENT APPLICATION NUMBER:

PRIOR APPLICATION NUMBER:

PRIOR FILING DATE: 2002-03-25

PRIOR FILING DATE:

NUMBER OF SEQ ID NOS: 4096

SOUTHWARE: Parentin Ver: 2.1

SEQ ID NO 3512
                                                                                                                                                                                                                                                                                                                   Length
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                                                                                                                                                                                                                                                                                                                                              Pred. No. 5.4e-130
5; Mismatches 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.5%; Score 495.5; DB 1
36.6%; Pred. No. 2.1e-40;
tive 53; Mismatches 118
                                                                                                                                                                                                                                                                                                             51.7%; Score 1387;
62.6%; Pred. No. 5.4
:ive 56; Mismatche
CURRENT FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: US 60/208,802
PRIOR FILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 68
                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-872-523-68
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409 MPSQERLDKFKVILISKRVGLRLEAADMCENQFICPATVKSVHGRLINVNFDGWDEEFDE 468
                                                                                                                                                                                                                                                                       APPLICANT: Davison, Eva M.
APPLICANT: Davison, Eva M.
APPLICANT: Lu, Xiaowei
TITLE OF INVENTION: A Tumor Suppressor Pathway in C. Elegans
FILE REFERENCE: 01997/536002
CURRENT APPLICATION NUMBER: US/09/872,523
CURRENT FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: US 60/208,802
BRICK FILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18.4%; Score 493.5; DB 10; Length 29.7%; Pred. No. 2.4e-40; ive 81; Mismatches 149; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EVVDKSQVSRTRMAVVDTVIGGRLR--LLYED-----GDSDDD----
                                           370 WVDCESPDIYPVGWCELTGYQLQPP 394
                                                                                    469 LYDVDSHDİLPIGWCEAHSYVLOPP 493
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                                                                                                                                                                                          Sequence 71, Application US/09872523
Patent No. US20020137906A1
GENERAL INFORMATION:
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Patent No. US20020137906A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-872-523-71
                                                                                                                                                                                                                                                         APPLICANT: Horvitz, H. Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 29.7%
Matches 132; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 71
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                                                                                                                                                                                                                                                                                     275 LEATQINAVPAKVFKWRLP-HGFLPNMKLEVVDKRNPRLIRVATIVDVDDQRVKVHFDGW 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---GFKVGMKLEAVDLMEPRLICVATVKRVVHRLLSIHFDGWDSEYDQ 369
  VIGGRLRLLYEDGDSDDDFWCHMWSPLIHPVGWSRRVGHGIKMSERRSDMAHHPT-FRK- 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 NCDSI---QVRWFARIEKVCGYRVIAQFIG----ADTKFWLNILSDDMFGLANAAMSDPN 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      245 FIFPVGFAAVNGYQLNAKKEYIEHTNKIAQAIKNGENPRYDSDDVTFDQLAKDPIDPMIW 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             206 KKVRAVYTEGGWFEEGMKLEAIDPL--NLGNICVATV---CKVLLDGYLMICVDGGPSTD 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              261 GLDWFCYHASSHAIFPATFCQKNDIELTPPKGYEAQTFNWENYLEKTKSKAAPSRLFNMD 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       353 -- DSFPIHINNTFMFPVGYAEKYNLELVPPDEFKG-TFRWDEYLEKESAETLPLDFLDLFK-P 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68
                                             ---HIPKGYRKD
                                                                                    ----AVPYLFKKVRAVYTEGGWFEEGMKLEAIDPLNLGNICVATVCKVL
                                                                                                               LDGYLMICVDGGPSTDGLDWFCYHASSHAIFPATFCQKNDIELTPPKGY-EAQTFNWENY
                                                                                                                                                                                                              219 ED-RILVHFDNW--DDSYDYWC-DVNSPYVQPVGWCQENGRTLIAPQGYPNPENFSWTEY
                                                                                                                                                                                                                                                       LEKTKSKAAPSRLFNMDCPNHGFKVGMKLEAVDLMEPRLICVATVKRVVHRLLSIHFDGW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           164 LIHPVGW------SRRVGHGIKMSERRSDMAHHPTFRKIYCDAV-PYLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 NSDAVLPSRVYWIASVIQTAGYRVLLRYEGFENDASHDFWCNLGTVDVHPIGWCAINSK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Davison, Ewa M.
APPLICANT: Lu, Kiaowei
TITLE OF INVENTION: A Tumor Suppressor Pathway in C. Elegans
FILE REFERENCE: 01997/536002
CURRENT APPLICATION NUMBER: US/09/872,523
CURRENT FILING DATE: 2001-06-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18.4%; Score 494.5; DB 10; Length 29.7%; Pred. No. 1.9e-40; ive 81; Mismatches 149; Indels
                                        VCGYRLRLHFDGYLSCYDFWTNAGSPDIHPVGWCEKTKHEL-
                                                                                                                                                                                                                                                                                                                                                                  364 DSEYDOWVDCESPDIYPVGWCELTGYOLOPP 394
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/208,802
PRIOR FILING DATE: 2000-06-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/09872523
Patent No. US20020137906A1
GENERAL INFORMATION:
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Best Local Similarity 29.7<sup>5</sup>
Matches 132; Conservative
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                                                                                                                                                                                                                                                        245 FIPPVGFAAVNGYQLNAKKEYIEHTNKIAQAIRNGENPRYDSDDVTPDQLAKDPIDPMIW
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                                                                                                         10 NSDAVLPSRVYWIASVIQTAGYRVLLRYEGFENDASHDFWCNLGTVDVHPIGWCAINSK-
                                                                                                                                                                                                                   ----ILVPPRTIHAKF-TDWKGYLMK----RLVGSRTLPVDFHIKMVESMKYPFRQGMRL
                                                      Gaps
                                                      83;
Length 498;
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Reb

-	Sequence 22, Appl	Sequence 32, Appl	Sequence 4752, Ap			1487,		14, A	365		Sequence 2394, Ap	Sequence 4205, Ap	4206,	Sequence 4207, Ap	Sequence 2393, Ap			Sequence 36, Appl	253	
	US-10-648-512-22	US-10-648-512-32	US-09-614-150A-4752	US-10-679-063-17795	US-10-425-114A-55600	US-60-495-114-1487	PCT-US03-30720-855	PCT-US02-14341-14	US-09-614-150A-36534	US-60-495-114-1488	US-60-500-337-2394	PCT-US03-28227-4205	PCT-US03-28227-4206	PCT-US03-28227-4207	US-60-500-337-2393	US-60-500-337-2396	US-09-614-150A-39579	US-10-275-762-36	PCT-US03-38193-2539	
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	94	94	93	93	92.5	92.5	92.5	92.5	92	92	90.5	90.5	90.5	90.5	90.5	90.5	90	90	90	
1	2.7	28	23	30	31	32	33	34	35	36	37	38	39	40	41	4.2	43	44	45	

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SAPLICANT: Venter, J. Craig

APPLICANT: Venter, J. Craig

APPLICANT: et al.

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: DETECTION EXPRESSION OF 10,000 OR MORE

TITLE OF INVENTION: DROSOPHILA GENES.

FILE REFERENCE: CLOOD78

CURRENT APPLICATION NUMBER: US/09/614,150A

CURRENT PILING DATE: 1000-07-11

PRIOR APPLICATION NUMBER: 60/160,191

PRIOR PILING DATE: 1999-10-05

PRIOR APPLICATION NUMBER: 60/160,332

PRIOR PILING DATE: 1999-11-12

PRIOR APPLICATION NUMBER: 60/161,932

PRIOR PILING DATE: 1999-11-12

PRIOR APPLICATION NUMBER: 60/164,769

PRIOR PILING DATE: 2000-01-12

PRIOR PILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: 60/113,383

PRIOR PILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: 60/194,831

PRIOR PILING DATE: 2000-02-24

PRIOR PILING DATE: 2000-03-33

NUMBER OF SEQ ID NOS: 430008

SOFTWARE: PRESEED FOR WINDOWN VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 277 AEVHSVGWCATRGKPLIPPRTIEHKYKDWKDFLVGRLSGARTLPSNFYNKINDSLQSRPR 336
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	OY 115 QGMRLEVVDKSQVSRTRMAVVDTVIGGRLRLLYEDGDSDDDWGHMMSPLIHFVGWSRRV 174  Db 689 LGLNLECVDKDRISQVRLATVTKIVGKRLFLRYFDSDDGFWCHEDSFIIHPVGWATTV 746	OY 175 GHGIKMSERRSDWAHHPTFRKIYCDAVPYLFKKVRAVYTEGGWFEE 220	QY 221 GMKLEAIDPLALGNICVATVCKVLLDGYLMICVDG-GPSTDGLDWFCYHASSHAIFPATF 279	QY 280 CQKNDIELTPPKGYEAQTFNWENYLEKTKSKAAPSRLFNMDCPNHGFKVGMKLEAVDLME 339	QY 340 PRLICVATVKRVVHRLLSIHFDGWDSEYDQWVDCESPDIYPVGWCELTGYQLQPP 394   :	Db 981 QQAPKPARPERTKKKKGPGKKRRIPPTKTRPLRQGSKKPLLEDDPQGARKISSE 453	Qy 454 PVPGEIIAVRVKEEHLDVASPDKASSPELPVSVENIKQETDD 495		; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF; FILE REFERENCE: CL001496; CURRENT APPLICATION NUMBER: US/10/719,993; CURRENT APPLICATION NUMBER: US/10/719,993; UNMERT FILING DATE: 2003-11-24; NUMBER OF SED ID NOS: 55342	; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 647 ; LENGTH: 894 ; TYPE: PRT ; ORGANISM: Homo sapiens	US-10-719-993-647  Query Match  Best Local Similarity 34.1%; Pred. No. 1.1e-37;  Matches 156; Conservative 65; Mismatches 170; Indels 66; Gaps 15;	QY 3 GMKVEVLNSDAVLPSRVXWIASVIQTAGYRVLLRXEGFENDASHDFWCNLGTVDVHPIGW 62	QY 63 CAINSKILVPPRTHAKFTDWKGYLWKRLVGSRTLPVDFHIKMVESMKYPFR 114	QY 115 -QGMRLEVVDKSQVSRTRMAVVDTVIGGRLRLLYBDGDSDDDFWCHMWSPLIHPVGW 170   :	171 SRRVGHGIRSDMAHHPTFRKIYCDAVPYIFKKVRAVYTE	Db 246 CQENKYRMDPPSEIXPLKMASEWKCTLEKSLIDAAKFPLFWEVFKDHADLRSH 298	Qy 215 GGWFEBGMKLEAIDPLNLGNICVATVCKVLLDGYLMICVDG-GPSTDGLDWFCYHASSHA 273	
:	Qy 175 GHGIKMSERRSDMAHHPTFRKIYCDAVPYLFKKVRAVYTEGGWFEE 220	QY 221 GMKLEAIDPINLGNICVATVCKYLLDGYLMICVDG-GPSTDGLDWFCYHASSHAIFPATF 279	QY 280 CQKNDIELTPPKGYEAQTFNWENYLEKTKSKAAPSRLFNWDCPNHGFKVGMKLEAVDLME 339	QY 340 PRLICVATVKRVVHRLLSIHFDGWDSBYDQWDCBSPDIYPVGWCELTGYQLQPP 394	QY 395 -VAAEPATPLKAKEATKKKKQPGKKRKRIPPTKTRPLRQGSKKPLLEDDPQGARKISSE 453   :	QY 454 PVPGEIIAVRVKEEHLDVASPDKASSPELPVSVENIKQETDD 495	RESULT 2 US-09-614-150A-27069 ; Sequence 27069, Application US/09614150A	<pre>/ GENERAL INFORMATION: / APPLICANT: Venter, J. Craig / APPLICANT: et al. / TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID / TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE / TITLE OF INVENTION: DROSOPHILA GENES.</pre>	CURRENT APPLICATION NUMBER: US/09/614,150A CURRENT FILING DATE: 2000-07-11 PRIOR APPLICATION NUMBER: 60/157,832 PRIOR PILING DATE: 1999-10-05 PRIOR APPLICATION NUMBER: 60/160,191	; PRIOR FILING DATE: 1999-10-19 ; PRIOR APPLICATION NUMBER: 60/161,932 ; PRIOR FILING DATE: 1999-10-28 ; PRIOR APPLICATION NUMBER: 60/164,769 ; PRIOR FILING DATE: 1999-11-12	PRIOR APPLICATION NUMBER: 60/173,383 PRIOR FILING DATE: 1999-12-28 PRIOR APPLICATION NUMBER: 60/175,693 PRIOR FILING DATE: 2000-01-12 PRIOR APPLICATION NUMBER: 60/184,831	FILING DATE: 2000-02-24 PELICATION NUMBER: 60/191,637 FILING DATE: 2000-03-23 OF SEQ ID NOS: 43008	FastSEQ for 7069 243	t: 4 4 8	Best Local Similarity 43.4%; Pred. No. 8.1e-75; Astches 234; Conservative 75; Mismatches 162; Indels 68; Gaps 14;	QY 3 GMKVEVLNSDAVLPSRVYWIASVIQIAGYRVLLRYEGFENDASHDFWCNLGT 54	570 GMKVEVENTDCDSIEVIQFGQTPTSFWVATILEIKGYKALMSYEGFDTD-SHDFWVNLCN 628 55 VDVHPIGWCAINSKILVPPRTIHAKFTDWKGYLMKRLVGSRTLPVDFHIKMVESMKYPFR 114	

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February 4, 2004, 09:05:51; Search time 20 Seconds (without alignments) 2380.175 Million cell updates/sec Run on:

US-10-031-915-36
2683
1 MKGMKVBVLNSDAVLPSRVY......KASSPELPVSVENIKQETDD 495 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	1 prot	ical		hypothetical prote	ribosomal protein	nebulin, skeletal	mating type silenc	DNA topoisomerase	DNA topoisomerase	polynucleotide ade	FIM protein [impor	polynucleotide ade	polynucleotide ade	microtubule-associ	neurofilament prot	6	hypothetical prote			hypothetical prote	₽	phosphoprotein pho	Cys-rich protein R	myosin-light-chain	unknown protein [i	histone H1 - maize	hypothetical prote	glutamate synthase	Ø
SUMMARIES	ΩΙ	T23964	25	T13797	T14794	F6421.7	S55024	T09481	G86586	D72038	S18642	T45119	S17875	S17925	A33319	B43427	T49475	F91286	B86128	F84912	T47381	T39004	T45058	T09483	JG0197	H86440	S26826	S	7043	5449
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	Length	619	711	1477	390	200	6999	1314	871	871	739	1379	689	740	721	332	756	1644	1644	701	1113	463	526	669	818	869	246	1285	1493	401
de	Query Match	00	17.6	'n	14.3								•	٠	•			•				•	٠	•		٠	•	•	3.4	3.4
	Score	494.5	7	402	384.5	16.	104	99.5	98	96	97.5	۲.	97	96.5	'n.	95	94	94	94	93	93	92.5	'n	92	92	92	ä	91.5	ij	91
	Result No.		7	m	4	Ŋ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53

321 CPNH------GFKVGMKLEAVDLMEPRLICVATVKRVVHRLLSIHFDGWDSEYDQ 369 

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hematopoietic line	hypothetical prote	protein F18014.25	related to gastric	zinc finger protei	hypothetical prote	histone H1, stress	neurofilament trip	cytochrome P450 AL	probable Na+/H+ an	neurofilament trip	membrane klotho pr	ankyrin 2, neurona	ftsK homolog - Str	histone H1, drough
S07633	T18738	H86327	T49813	S27802	T19450	T07035	Огнин	JS0724	E84431	A43427	JC5925	837431	T35683	865059
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486	803	1314	1331	2150	2150	207	1020	510	1162	909	1012	3924	929	202
ω ι. 4. 4	. 4.	3.4	3.4	3.4	3.4	3.4	3.4	3.3	3.3	3.3	3.3	3.3	3.3	3.3
4 5	90.5	90.5	90.5	90.5	90.5	90	90	89.5	89.5	8	89	88	88.5	88
30	35	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1 T23964 Ly23964 Ly23964 Ly23964 Ly23964 Ly23964 Ly23964 Ly23964 Ly23964 Ly23061 Ly3061  RESULT 1 T23964 Mypothetical protein RO6C7.7 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T23964 R;Gardner, A. Submitted to the EMBL Data Library, April 1996	A; Accession: 123964 A; Accatus: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Residues: 1-619 <wil> A; Residues: 1-619 <wil> A; Residues: 1-619 <wil> A; Experimental source: Clone R06C7 C; Genetics: CESP:R06C7.7 A; Genetics: As a constant of the co</wil></wil></wil>	ch 18 Similarity 29.7%; Pred. No. 2.1e-33; Length 619; 132; Conservative 81; Mismatches 149; Indels 83; Gaps 18;	10 NSDAVLPSRVYWIASVIQTAGYRVLLRYEGFENDASHDFWCNLGTVDVHPIGWCAINSK- 68	69ILVPPRTIHAKF-TDWKGYLMKRLVGSRTLPVDFHIKAVJESMKYPFRÇGMRL 119 	120 EVVDKSQVSRTRMAVVDTVIGGRLRLLYEDGDSDDDFWGHMWSP 163	164 LIHPVGWSRRVGHGIKMSERRSDWAHHPTFRKIYCDAV-PYLF 205	206 KKVRAVYTEGGWFEEGMKLEAIDPLNLGNICVATVCKVLLDGYLMICVDGGFSTD 260	261 GLDWFCYHASSHAIFPATFCQKNDIELTPPKGYEAQTFNWENYLEKTKSKAAPSRLFNMD 320 	
	RESULT 1 123964 hypothetical protein C.Species: Caenorhai C.Jate: 15-Oct-1999 C.Accession: T23964 Rydardner: A. A. Submitted to the EMI A.Reference number:	As Accession: 1239 As Status: prelimir As Molecule type: 1 As Residues: 1-619 As Experimental son C; Genetics: cESP: Ro6C; As Agene: cESP: Ro6C; As Map position: 1 As Introns: 121/3;	# D	т					

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LEVVDKSQVSRTRMAVVDTVIGGRLRLLYEDGDSDDFWCHMWSPLIHPVGWSRRVGHGI 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   299 NWENYLEKTKSKAAPSRLFNMDCPNHGFKVGMKLEAVDLMEPRLICVATVKRVVHRLLSI 358
                                                                                                                                                                                                                                                                                                                                                                                       CAINSKILVPPRTIHAKFTDWKGYLMKRLVGSRTLP--VDFHIKMVESM--KYPFRQGMR 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein DKFZp586P1522.1 - human
C;Species: Homo sapiens (man)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
                    A,Cross-references: EMBL:X80839; NID:g530289; PIDN:CAA56811.1; PID:g3421009
C,Genetics:
A,Cross-references: FlyBase:FBgn0002441
A,Introns: 210/3; 746/1
                                                                                                                                                                                                                                                                                                                                                                                                                                         908 CDETARVLQAPKDYNSERFSWSRYLVK--TGGKAAPRALFGHLNMOQQMDVRNGPAVGMH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            239 TVCKVLLDGYLMICVDGGPSTDGLDWFCYHASSHAIFPATFCQKNDIELTPPKGYEAQTF
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                                                                                                                                                                                                                                                                                                             1018 -----HEGRO------
                                                                                                                                                                                                                                                                            3 GMKVEVINSDAVLPSRVYWIASVIQTAGYRVILRYEGFENDASHDFWCNLGTVDVHPIGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----EIVYPKVAE----VVQAKRKTSPCEEKVVKKQKQMQKEED 1253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HFDGWDSEYDQWVDCESPDIYPVGWCELTGYQLQ-PPVAAEPATPLKA-------
                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        443 DPQGARKISSEPVPGEIIAVRVKEEHLDVASPDKASSP--ELPVSVENIKQETDD 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     966 LEAEDLNDTGKICVATVTDILDERIRVHFDGWDDCYDLWVHITSPYIHPCGW----
                                                                                                                                                            Ouery Match 15.0%; Score 402; DB 2; Length 1477; Best Local Similarity 21.9%; Pred. No. 4e-25; Matches 117; Conservative 83; Mismatches 159; Indels 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39;
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R;Kochrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, submitted to the Protein Sequence Database, August 1999

A;Reference number: Z18180

A;Accession: T14794

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-390 < KOE>

A;Cross-references: EMBL:AL110279
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C;Genetics:
A;Note: DKFZp586P1522.1
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Best Local Similarity 36.2%
Matches 94; Conservative
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C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C;Accession: T13797
R;Wismar, J; Loeffler, T; Habtemichael, N.; Vef, O.; Geissen, M.; Zirwes, R.; Altmeyer
R;Wismar, J; Loeffler, T; Habtemichael, N.; Vef, O.; Geissen, M.; Zirwes, R.; Altmeyer
A;Title: The Drosophia melanogaster tumor suppressor gene lethal(3)malignant brain tumor
A;Reference number: Z17760; MUID:96100389; PMID:8555106
A;Accession: T13797
A;Accession: T13797
A;Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 AFQDSLSTWIVTVVENIGGRLKLRYEGLESSDNYEHWLYYLDPFLHHVGWAAQQGYELQP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 NSKILVPPRTIHAKFIDWKGYLMKRLVGSRTLPVDFHIKMVESMKYP---FRQGMRLEVV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            231 NLGNICVATVCKVLLDGYLMICVDG-GPSTDGLDWFCYHASSHAIFPATFCQKNDIELTP 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PKGYEAQTFNWENYLEKTKSKAAPSRLFNMDCPNHGFKVGMKLEAVDLMEPRLICVATVK 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RVVHRLLSIHFDGWDSEYDOW-VDCESPDIYPVGWCELTGYQLQPPVAAEPATPLKAKEA 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      347 YKORKIAVVOPEKOVPSSRT--VHEGLRN------ÓBLNSTEŠVMINGKYCCPKIYFNH 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59
                                                                                                                                                                                                                    Species: Homo sapiens (man)
Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 NKKTLEAPEGIRDKVSDWDEFLRQTLIGACSPPVPL-LEGLRNGRNPLDLIAPGSRLECQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 PSAIRHLKNEAEWQEILAKVKEEEBEPLPSYLFKDKQVIGIHT-+--FSVNMKLEAVDPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 DKSQVSRTRMAVVDTVIGGRLRLLYEDGDSDDDF---WCHMWSPLIHPVGWSRRVGHGIKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 SERRSDMAHHPTFRKIYC-----DAVP-YLF--KKVRAVYTEGGWFEEGMKLEAIDPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                              hypothetical protein DKPZp434L243.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: T12525
R;Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, June 1999
A;Reference number: 217524
A;Accession: T12525
A;Retaus: prefininary
A;Molecule type: mRNA
A;Residues: 1-711 «WAM
A;Residues: 1-711 «WAM
A;Residues: 1-711 «WAM
A;Residues: 1-712 «WAM
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A;Residues: 1-715 «WAM
A;Residues: 1-715 «WAM
A;Roberimental source: adult testis; clone DKFZp434L243
C;Genetics:
A;Note: DKFZp434L243.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17.6%; Score 471; DB 2; Length 711; 30.2%; Pred. No. 2.4e-31; ive 79; Mismatches 186; Indels
394
                                590 LYDVDSHDILPIGWCEAHSYVLQPP 614
370 WVDCESPDIYPVGWCELTGYQLQPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              469 LDVASP--DKASSPELPVSV 486
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Best Local Similarity 30.2°
Matches 133; Conservative
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                                                                                   February 4, 2004, 09:05:51; Search time 39 Seconds (without alignments) 3275.283 Million cell updates/sec
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                                                                                                                                                            2683
1 MKGMKVEVLNSDAVLPSRVY......KASSPELPVSVENIKQETDD 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
                                                                                                                                                                                                                                                                                830525
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                   830525 seqs, 258052604 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                     OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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09VX33
08C1B4
096C73
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Q8IUV7
Q21769
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Q8BZY2
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Q9JMD1
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Gapop 10.0 , Gapext 0.5
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sp_unclassified:*
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sp_human:*
sp_invertebrate:*
sp_mammal:*
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sp_bacteriap:*
sp_archeap:*
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                                                                                                                                                                                                                                                                                                                                                                                                                SPTREMBL 23:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
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Maximum DB seq length: 200000000
                                                                                                                                              US-10-031-915-36
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sp_rodent:*
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Match Length DB
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Perfect score:
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## ALIGNMENTS

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243 RKVLADGFLMIGIDGSBAADGSDWFCYHATSPSIFPVGFCEINMIELTPPRGYTKLPFKW 302
                                                                                                     DGWDSBYDQWVDCESPDIYPVGWCELTGYQLQPPVAAEPATPLKAKEATKKK-KKQFGKK 419
                                                                                                                                                                                            VDKSQVSRTRMAVVDTVIGGRLRLLYEDG-DSDDDFWCHMWSPLIHPVGWSRRVGHGIKM 180
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                                                                        ENYLEKTKSKAAPSRLFNMDCPNHGFKVGMKLEAVDLMEPRLICVATVKRVVHRLLSIHF
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MEDINE=235354683; PubMed=12466851;
The FANTOM CONSortium,
The RANTOM Consortium,
The RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of the Marty Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Coloration Colorat
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                      420 RKRIPPTKTRPLRQGSKKPLLEDDPQGARKISSEPVPGEIIAVRVKEE
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52.1%; Score 1398; DB 11; 62.9%; Pred. No. 7.5e-125; ive 56; Mismatches 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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COCALL,
COLMAR-2003 (TEMBLE). 23,
COLMAR-2003 (TEMBLE). 23,
COLMAR-2003 (TEMBLE). 23,
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331 VVDKTQVSRTRMAVVDTVIGGRLRLLYEDGDSDDDFWCHMWSPLIHPVGWSRRVGHGIKM 390
                                                                        CKVLLDGYLMICVDGGPSTDGLDWFCYHASSHAIFPATFCQKNDIELTPPKGYEAQTFNW 300
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                                           SERRSDMAHHPTFRKIYCDAVPYLFKKVRAVYTEGGWFEEGMKLEAIDPLNLGNICVATV
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Mus.
MCBI_TaxID=10090,
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC020018; AAH20018.1;
MGD; MGI:2143977; AA408199.
InterPro; IPR004092; Mbt.
Pfam; PF02820; mbt; 4.
SMART; SM00561; MBT; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
SEQUENCE 464 AA; 52721 MW; 31E5C041592BE874 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2002 (TrEMBLrel. 20, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Similar to hypothetical protein FLJ20055.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52.9%; Score 1418; DB 11;
56.4%; Pred. No. 1.1e-126;
cive 67; Mismatches 121;
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689 QLPLPIESIKQERNN 703
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Ephydroidea; Drosophilidae; Drosophila
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InterPro; IPR001660; SAM.
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Pfam; PF00536; SAM; 1.
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SMART; SM00454; SAM; 1
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           NCBI TaxID=7227;
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EMBL; AE003639;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 VDKSQVSRIRMAVVDTVIGGRIRLLYEDG-DSDDDFWCHMWSPLIHPVGWSRRVGHGIKM 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SERRSDMAHHPTFRKIYCDAVPYLFKKVRAVYTEGGWFEEGMKLEAIDPLNLGNICVATV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            190 SDITKKODGH------FDTPPHLPAKVKEVDQSGEWFKEGMKLEAIDPLNLSTICVATI 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CKVLLDGYLMICVDGGPSTDGLDWFCYHASSHAIFPATFCQKNDIELTPPKGYEAQTFNW 300
                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                    KGMKVEVLNSDAVLPSRVYWIASVIQTAGYRVLLRYEGFENDASHDFWCNLGTVDVHPIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243 RKVLADGFLMIGIDGSEAADGSDWFCYHATSPSIFPVGFCEINMIELTPPRGYTKLJPFKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    303 FDYLRETGSIAAPVKLFNKDVPNHGFRVGMKLEAVDLMEPRLICVATVTRIIHRLLRIHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 ENYLEKTKSKAAPSRLFNMDCPNHGFKVGMKLEAVDLMEPRLICVATVKRVVHRLLSIHF
                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                      Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tandka T., Nakamura Y., Isogai T., Sugano S.;
"NEDO human cDNA sequencing project.";
Submitted (FEB-2000) to the EMEL/GenBank/DDBJ databases.
EMBL; AK000062; BAA90919.1;
                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                  8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                      / Match 52.0%; Score 1395; DB 4; Length 410; Local Similarity 62.9%; Pred. No. 1.4e-124; less 249; Conservative 55; Mismatches 84; Indels
                                                                                                                                                                                                                                                            InterPro; IPR004092; Mbt.
Pfam; PF02820; mbt; 4.
MART; SM00561; MBT; 4.
Hypochetical protein.
SEQUENCE 410 AA; 46717 MW; 6E9C09639AC02CF3 CRC64;
                                                     01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OAT-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein FLJ20055.
Homo sapiens (Human).
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 DGWDSEYDQWVDCESPDIYPVGWCELTGYQLQPPVA 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DGWEEEYDOWVDCESPDLYPVGWCQLTGYOLOPPAS 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1243 AA.
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                                PRT;
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                               PRELIMINARY;
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                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                     NCBI_TaxiD=9606;
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                                                                                                                                                                                                                                                                                                                                        Query Match
                                          LUXN60
                             O9NXU1
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RESTORANCE FROM N.A. (LUDUG AND SHORT ISOFGRANS).

REY STUCIALE FROM N.A. (LUDUG AND SHORT ISOFGRANS).

REY Adams M.D. (Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adams M.D., Celniker S.E., Holt R.A., Rabburner M., Henderson S.N., Butch G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Guerge R.A., Devis S.E., Richards S.C., Abburner M., Henderson S.N., Butch G., Baradon R.C., Ragars Y.H.C., Blazel R.G., Champe M., Pichifer B.D., Fan R.H., Doyle C., Barkendale J., Bayraktaroglu L., Besaley E.M., Ballew R.M., Bassu A., Barachale J., Bayraktaroglu L., Besaley E.M., Ballew R.W., Bansu A., Barachale J., Bayraktaroglu L., Besaley E.M., Ballew R.W., Bansu D.A., Devis D., Butcher M., Cawley S., Daller H., Cadieu E., Cener A., Chandra I., Berlow B. D., Detcher M., Cawley S., Dalle C., Ferraz C., Errites B., Chandra I., Berlow B. D., Detcher M., Deng Z., Mays A.D., Dew I., Diez S.M., Activer J. Devis B. Detcher M., Dengar-Rochas S., Dunkow B.C., Dunn P., Dutchin K.J., Evangelista C.C., Ferraz C., Ferraz C., Ferraz C., Stanson D.K., Harrey D., Henman T.J., Hermandez J.R., Houck J., R. Harris N.L., Harrey D., Henman T.J., Hermandez J.R., Houck J., Stanson D.L., Houston K.A., Howland T.J., Mei M.H., Ibeger C., Maris D., Lai Z., Liang Y., Lin X., Mallsh F., Karpen G.H., Ke Z., Kennison J.A., Nelson D.L., Ra Mount S.M., Molostry C., Moristy D.M., Nelson D.L., Raken M. Mustan D.M., Nelson D.L., Malson D.L., Manner B., Manner B., Wang C., Stden-Kiamos I. S., Randers R.D.C., Scheeler F., Schen H., Wang Sarleksen D.M., Pittman G.S., Pan S., Pollard J., Pull J., Manner B., Manner E.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       529 AEVHSVGWCATRGKPLIPPRTIEHKYKDWKDFLVGRLSGARTLPSNFYNKINDSLQSRFR 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 VDVHPIGWCAINSKILVPPRTIHAKFIDWKGYLMKRLVGSRILPVDFHIKMVESMKYPFR 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115 QGMRLEVVDKSQVSRTRMAVVDTVIGGRLRLLYEDGDSDDDFWCHMWSFLIHPVGWSRRV 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   570 GMKVEVENTDCDSIEVIQPGQTPTSFWVATILEIKGYKALMSYEGFDTD-SHDFWVNLCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 GMKVEVLNSD-----AVLPSRV---YWIASVIQTAGYRVLLRYEGFENDASHDFWCNLGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41.4%; Score 1111; DB 5; Length 1
43.4%; Pred. No. 9.7e-97;
ive 75; Mismatches 162; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PSS0105; SAM_DOMAIN; 1.
Alternative splicing; Hypothetical protein.
VARSPLIC MISSING (IN SHORT ISOFORM).
SEQUENCE 1243 AA; 136036 MW; 35FC45F6298F5BAA_CRC64;
(LONG AND SHORT ISOFORMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FlyBase; FBgn0032475; CG16975
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14;

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62 WCAINSKILVPPRTIHAKFTDWKGYLMKRLVGSRTLPVDFHIKMVESMKYP---FRQGMR 118
   337 LMEPRLICVATVKRVVHRLLSIHFDGWDSEYDQWVDCESPDIYPVGWCELTGYQLQPPVA 396
                                                             397 AEPATPLKAKEATKKK-KKQFGKKRKRIPPTKTRPLRQGSKKPLLEDDPQGARKISSEPV 455
                                                                                       294 QSSRESQSASSKQKKKAKSQQXKGHKKMTTSQL-----KEELLDGEDYSFLHGASDQE 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :|| : || || || || : ::|
284 VDPWSPFGISPATVVKVFDEKYFLVEMDDIRPENHARRSFVCHADSPGIFPVQWSLKNGL 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          344 HISPPPGYPSQDFDWADYLKQCGABAAPQRCFPPLISEHEFKENMKLEAVNPILPEEVCV 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATVKRYVHRLLSIHFDGWDSEYDQW-VDCESPDIYPVGWCELTGYQLQPPVAAEPATPLK 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AKEATKKKKKOFGKKRKRIPPTKTRPLROGSKKPLLEDDPOGARKISSEPVPGEIIAVRV 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 234 LMEPRLICVATVTRIHRLLRIHFDGWEEEYDGWVDCESPDLYPVGWCQLTGYQLQPPAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 GMKVEV-LNSDAVLPSRVYWIASVIQTAGYRVLLRYEGFENDASHDFWCNLGTVDVHPIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LEVVDKSQVSRTRMAVVDTVIGGRLRLLYEDGDSDDDF--WCHMWSPLIHPVGWSRRVGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GIKMSERRSDMAHHPTFRKIYC-----DAVP-YLF--KKVRAVYTEGGWFEEGMKLEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           227 IDPLNLGNICVATVCKVLLDGYLMICVDG-GPSTDGLDWFCYHASSHAIFPATFCQKNDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     286 ELIPPKGYEAQTFNWENYLEKTKSKAAPSRLFNMDCPNHGFKVGMKLEAVDLMEPRLICV
                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   404 ATITAVRGSYLWLOLEGSKKPIPECIVSVESMDIPPLGWCETNGHPL---
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                                                                                                                                                                                                                                                                                                                                                                                                                            Straubberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
BMBL, BC014614, AAH14614.1;
InterPro; IPR004092; Mbt.
InterPro; IPR004092; Mbt.
Pfam; PF00280; mbt; 4.
Pfam; PF00586; SAM; 1.
SMART; SM00561; MBT; 4.
SMART; SM00454; SAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    866 AA; 98141 MW; DCE67BF35C413EB7 CRC64;
                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23.1%; Score 620.5; DB 4;
larity 31.9%; Pred. No. 4.3e-50;
Conservative 91; Mismatches 205;
                                                                                                                                                                                                                                866 AA
                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                       PGEIIAVRVKEE 467
                                                                                                                                                   SNGSATVYIKOE 358
                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                        Similar to RU1.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 161; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. TISSUE=Muscle;
                                                                                                                         456
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                                                                                                                                                                                                                                                 -VAAEPATPLKAKEATKKKKQFGKKRKRIPPTKTRPLRQGSKKPLLEDDPQGARKISSE 453
                                                                                                                                                                                                                                                                                                                                                                        :| | : | | : | | : | | 1029 -LPKLSIKLEHRNAAFYENNQPEEEGDEEDPDADGDGDGSTSHISEQSTTQSSSD 1086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        216
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annotation of
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                                                                                                                                                                   COKNDIELTPPKGYEAQTFNWENYLEKTKSKAAPSRLFNMDCPNHGFKVGMKLEAVDLME
                                                                                                                                                                                                                             PRLICVATVKRVVHRLLSIHFDGWDSEYDQWVDCESPDIYPVGWCELTGYQLQPP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WFEEGWKLEAIDPLNLGNICVATVCKVLLDGYLMICVDGGPSTDGLDWFCYHASSHAIFP
                                             GHGI------KVRAVYTEG--GWFEE
                                                                                                                                      GMKLEAVDPLNLSSICPATVMAVLKFGYMMIRIDSYQPDASGSDWFCYHEKSPCIFPAGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       157 WCHMWSPLIHPVGWSRRVGHGIKMSERRSDMAHHPTFRKIYCDAVPYLFKKVRAVYTEGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98 PVDFHIKMVESMKYPFRQGMRLEVVDKSQVSRTRMAVVDTVIGGRLRLLYEDG-DSDDDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 PPDFSQKVSESMQYPFKPCMRVEVVDKRHLCRTRVAVVESVIGGRLRLVYEESEDRIDDF
                                                                                                                                                                                                                                                                                                                                                     PVPGEIIAVRVKKEHLDVA----SPDKASSPELP-----VSVENIKQETDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                      981 QOAPKPAPKPKIQRKRKPKKGAAGGK----TPTDNNTQSVKSRTIALKTTPH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 1079; DB 11; Length 359;
; Pred. No. 1.9e-94;
45; Mismatches 102; Indels 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=C57BL/6J; T1SSUE=Skin;
MFDLINE=22354683; PubMed=12466851;
The FANTOM CONSORtium,
the RIKEN Genome Exploration Research Group Phase I & II
"Analysis of the mouse transcriptome based on functional
60,770 full-length cDNAs.";
Nature 420:533-573(2002).
EMBL; AK028503; BAC25982.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CA233E1B6B60CA04 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 23, Created)
(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2003 (TrEMBLrel, 23, Last
Weakly similar to H-L (Fragment)
Mus musculus (Mouse).
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Best Local Similarity 56.2%;
Matches 209; Conservative 49
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Sequence 26098, A Sequence 701, App Sequence 1042, App Sequence 104678, Sequence 111883, Sequence 103678,

Sequence 111883, Sequence 4056, Ap Sequence 13849, A Sequence 13758, A Sequence 1597, Ap Sequence 1597, Ap Sequence 9205, Ap Sequence 25887, A Sequence 25887, A Sequence 25827, A Sequence 2582, Ap Sequence 2582, Ap Sequence 5856, App Sequence 5856, App Sequence 5856, App Sequence 586, Appli Sequence 588, Appli Sequen

Sequence 137841, Sequence 137842, Sequence 137841,

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1 AGCACGTCCCACTCTATGACCAGTGGGAGGATGTGAAAGGGATGAAGGTGGAGGTGC
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Sequence 622, Application US/10117722

Publication No. US20030219744A1

SERNEAL INFORMATION:

APPLICANT: Tang, Y. Tom

APPLICANT: Tang, V. Tom

APPLICANT: Liu, Chenghua

APPLICANT: Aband, Junod

APPLICANT: Aband, Junod

APPLICANT: Drmanac, Radoje T.

PRICE REFERENCE: 784CIP2BCIP POLJON 17, 722

CURRENT FILING DATE: 2002-04-04

PRICE PLING DATE: 2000-07-19

PRICE PRICE APPLICATION NUMBER: 09/488, 725

PRICE PRICE APPLICANTION NUMBER: 09/488, 725

PRICE PRICE PRICE DROS: 1104

SOFTWARE DF. EL-Genes Version 1.0

SEQ ID NO 622

ENDRE PRICE PRICE PRICE DROS: 1104

MUMBER OF SEQ ID NO 621

ENDRE PRICE PRICE PRICE DROS: 1104

ENDRE PRICE PRICE DROS: 1104

SED ID NO 622

ENDRE PRICE PRICE DROS: 1104

1 US-09-918-995-26775
11 US-09-918-995-26698
12 US-00-918-995-26698
13 US-10-029-86-1701-701
13 US-10-029-86-186-183
14 US-10-027-632-103678
14 US-10-027-632-111883
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99.8%; Score 2550.8;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2552; Conservative 0; Mismatches
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ORGANISM: Homo sapiens
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Sequence 621, App
Sequence 419, App
Sequence 1068, Ap
Sequence 70682, A
Sequence 70682, A
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sequence 55, Appl
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2: /cgn2_6/ptodata/1/pubpna/PET_IBMP_PUBL.seq:*
3: /cgn2_6/ptodata/1/pubpna/DS0_NEW_PUB.seq:*
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5 US-10-037-270-622

3 US-10-094-749-917

9 US-10-064-237-419

2 US-10-108-260A-1658

3 US-10-027-632-70682

4 US-10-027-632-70683

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Maximum Match 100%
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1020 1007 1187 1247 1081 AACGAGTGGTGCATCGGCTCCTCAGCATCCACTTTGACGGCTGGGACAGCGAGTACGACC 1140 1008 TGATGATCTGTGTGGACGGGGGCCCTCCACAGATGGCTTGGACTGGTTCTGCTACCATG 1067 1068 CCTCTTCCCACGCCATCTTCCCGGCCACCTTCTGTCAGAAGAATGACATTGAGCTCACAC 1127 AACGAGTIGGTGCATCGGCTCCTCAGCATCCACTTTGACGGCTGGGACAGCGAGTACGACT 1367 407 240 467 300 360 587 420 647 480 707 540 780 840 900 960 228 AGCACGTCCCACTCTATGACCAGTGGGAGGATGTGATGAAAGGGATGAAGGTGGAGGTG 767 900 827 601 ATCACCCCACCTTCCGGAAGATCTACTGTGATGCCGTTCCTTACCTCTTCAAGAAGGTAC 660 661 GAGCAGTCTACACAGAAGGCGGTTGGTTTGAGGAAGGGATGAAGCTGGAGGCCATTGACC 720 947 828 ATCACCCCACCTTCCGGAAGATCTACTGTGATGCCGTTCCTTACCTCTTCAAGAAGGTAC 887 GGTGCAACCTGGGAACAGTGGATGTCCACCCCATTGGCTGGTGTGCCATCAACAGCAAGA TCCTAGTGCCCCCACGACCATCCATGCCAAGTTCACCGACTGGAAGGGCTACCTCATGA recraencececcacearceareceareceaerreaceaerregaaeeeerracerea 528 AACGGCTGGTGGGCTCCAGGACGCTTCCCGTGGATTTCCACATCAAGATGGTGGAGGAGCA 708 Arderdacadreaceaceacricidereccacarerdadecececerdarecaceaged 768 GTTGGTCACGACGTGTGGGCCACGGCATCAAGATGTCAGAGAGGCGAAGTGACATGGCCC TCAACAGTGATGCTGTGCTCCCCAGCCGGGTGTACTGGATCGCCTCTGTCATCCAGACAG 348 CAGGGTATCGGTGCTTCGGTATGAAGGCTTTGAAAATGACGCCAGGCCATGACTTCT AACGGCTGGTGGCTCCAGGACGCTTCCCGTGGATTTCCACATCAAGATGGTGGAGAGAA TGAAGTACCCCTTTAGGCAGGCATGCGCTGGAAGTGGTGGACAAGTCCCCAGGTGTCAC 421 GCACTCGCATGGCTGTGGTGGACACAGTAATCGGGGTCGCCTACGGCTCCTCTACGAGG TGAAGTACCCCTTTTAGGCAGGCATGCGGCTGGAAGTGGTGGACAAGTCCCAGGTGTCAC 648 GCACTCGCATGGCTGTGGTGGACACAGTAATCGGGGGTCGCCTACGGCTCCTCTACGAGG 481 ATGGTGACAGTGACGACGACTTCTGGTGCCACATGTGGAGCCCCCTGATCCACCCAGTGG GTTGGTCACGACGTGTGGGCCACGGCATCAAGATGTCAGAGAGGCGAAGTGACATGGCCC 961 CGAAAGCCGCTCCATCGAGACTCTTTAACATGGATTGCCCAAACCATGGCTTCAAGGTGG 888 GAGCAGTCTACACACACACGCGGTTGGTTTGAGGAAGGGATGAAGCTGGAGGCCATTGACC 841 CCTCTTCCCACGCCATCTTCCCGGCCACCTTCTGTCAGAAGAATGACATTGAGCTCACAC 901 GGCCAAAAGGTTATGAGGCACAGACTTTCAACTGGGAGAACTACTTGGAGAAGACCAAGT 1188 ceaaaccarccarccarcrrrraacarcearraccaaaccaraccaraccara GCATGAAGCTGGAGCCGTGGACCTGATGGAGCCCCGGCTCATCTGTGTGGCCCACGGTGA 781 TGATGATCTGTGTGGACGGGGCCCTCCACAGATGGCTTGGACTGGTTCTGCTACCATG 1128 GGCCAAAAGGTTATGAGGCACAGACTTTCAACTGGGAGAACTACTTGGAGAAGACCAAGT

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1141   AGTGGGTGGACTGCGAGCTCTACCCCGTCGGCTGGTGTGAGCTCACCGGCT   1200   1368   AGTGGGTGGACTGCCGAGCTTACCCCGTCGGCTGGTGTGTGAGCTCACCGGCT   1427   1201   ACCAGCTCCAGCGTCTGCGAGCCCACCGGCT   1427   1201   ACCAGCTCCAGCGCTCGTGGCCACCGCTGGCTGTGAGGCCACCGGCT   1428   ACCAGCTCCAGCCCCCAGCAGCCCACCGCCACCGCCACCGCCAAGAGGCCA   1487   1261   CAAAGAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1501 TCAAGCAGGAAACAGACTGAGCCTTCCTGCCTCCAGCCTGGAAGCC 1560 1728 TCAAGCAGGAAACAGACTGAGCCTTCCTGCTCCAGCCTTGACTCGAAGCC 1787 1561 AGCCCAGGGTTTTCTACCACCACCACCACCTCGACTTTGGCTTGGAAACCC 1787 1788 AGCCCAGCGTTTTCTTACCACCACCACCACCCTGACTTTGGCTTGGAAACTGA 1620 1788 AGCCCAGCGTTTTCTTACCACCACCACCACCACCTGACTTTGGCTTGGAAACTGA 1847 1621 TCCTCTCTGTGAAATTCTGCCCGCTGCTGAAGCTGGAAGGTTTGGCTTGGAACTGA 1847 1621 TCCTCTCTGTGAAAATTCTGCCCGGTGCTGTGAAGGCTGGAAGGACTGCTGGAGGACTGA 1977 1681 GTCTCTGTGGAAATTCTGCCCGGTGCTGTGAAGGCTGGAAGGACTGCTGGGGG 1907 1681 GTCTCCTGGGAACCCGCTGTTGGTTGTGAAGGCTGGAAGGTCTATATGACGGG 1907 1741 CGCTGGAACTCGTTGTGAACCACCTTTTCCAGCAGAGTCTATATGACGGGC 1967 1741 CGCTGAGGACCCCAGAACTTCTGAAACCACCTTTTCCAGCCAG	TIGCCAGGGATGGGGCCACCTCTCACACTGTGGAATACAAGACAGTGAACTCTGTCTG	ZIBI CCIIGAGCIGCIIICIGIGIIIGIGAGGGCIGACICCCAIIICCIAAAGGAAAIGCCCCC ZZZU Z388 CCIIGAGCIGCTITCIGIGIIIGIGAGGGACIGACICCCAIIICCIAAAGGAAAIGCCCCC 2447

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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PAI31P1
CURRENT APPLICATION NUMBER: US/10/264,237
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/16450
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PRIOR FILING DATE: 2001-05-18
PRIOR FILING DATE: 2000-05-19
SPRIOR FILING DATE: 2000-05-19
SOFTWARE: PATENTION NUMBER: US 60/205,515
SOFTWARE: PATENTION NUMBER: 3.1
SEQ ID NO 419
: LENGTH: 2663
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                     GAAGCCCCGCTAAAATAATTCATCCAAGATTCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                          2521 AATTAAACCCCTGCTTGCTTG 2542
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AATTAAACCCCCTGCTTGCTTG 3188
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Publication No. US20040009491A1
GENERAL INFORMATION:
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NAME/KEY: misc_feature
LOCATION: (775)..(775)
OTHER INFORMATION: n equals a,t,g,
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1 LOCATION: (2662)...(2662)

2 OTHER INFORMATION: n equals a,t,g,

US-10-264-237-419
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MISC FEATURE
LOCATION: (1248)
OTHER INFORMATION: n equals a,t,g,
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LOCATION: (2648) . (2648)
OTHER INFORMATION: n equals a,t,g,
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LOCATION: (660)..(660)
OTHER INFORMATION: n equals
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LOCATION: (1824)..(1824)
OTHER INFORMATION: n equals
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LOCATION: (2642)..(2642)
OTHER INFORMATION: n equals
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ORGANISM: Homo sapiens
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TGGAACGCTAGCTGCTCTTCCTTAAGATGGCCTCCCCCGACCCGCACGCCACGGCCCTC 1858
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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION UNMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR PLING DATE: 2000-07-20
PRIOR PLING DATE: 2000-04-20
PRIOR PLING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PRILING DATE: 2000-02-24
PRIOR PRILING DATE: 2000-02-24
PRIOR PLING DATE: 2000-02-24
PRIOR PLING DATE: 1999-10-23
PRIOR PLING DATE: 1999-10-23
PRIOR PLING DATE: 1999-10-28
PRIOR PLING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARR: FABSERQ FOR WINDOWS VERBION 4.0
SERVINGER: 513
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Publication No. US20030204075A9
GENERAL INFORMATION:
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Best Local Similarity 99.6%;
Matches 511; Conservative
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; ORGANISM: Human
US-10-027-632-70682
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       RESULT 6
10s-10-027-632-70682
10s-10-027-632-70682, Application US/10027632
10s-10-027-632-70682, Application US/10027632
10sequence 70682, Application US/20030204075A9
10seption No. US20030204075A9
10seption No. US2
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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR PLING DATE: 2000-07-12
PRIOR PLING DATE: 2000-04-20
PRIOR PELING DATE: 2000-04-20
PRIOR PELING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR PILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR PLILNG DATE: 1999-10-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR PRILNG DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-09
NUMBER OF SEQ ID NOS: 325720
SOFTHARE: PRESESEQ FOR WINDOWS VERSION 4.0
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Best Local Similarity 99.6
Matches 511; Conservative
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US-10-027-632-70682
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US-10-027-632-70683
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LENGTH: 513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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Pred. No. 1e-147;
2; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1439 TCTAGACGTGGCCTCGCCCGACAAGGCTTCAAGTCCAGAGCTGCCTG
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                                                                   PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/199,676
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 1999-11-23
PRIOR PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-09-28
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US-10-027-632-70683
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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TILE REPERENCE: 108827,129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-02-34
PRIOR PRIOR DATE: 2000-02-34
PRIOR PILING DATE: 2000-02-34
PRIOR PILING DATE: 1900-02-34
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-11-33
PRIOR PILING DATE: 1999-02-8
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-09
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; ORGANISM: Human
US-10-027-632-293974
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Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
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Pred. No. 1e-147;
2; Mismatches 0; Indels 0;
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20.0%; Score 512.2;
Best Local Similarity 99.6%; Pred. No. 1e-1
Matches 511; Conservative 2; Mismatches
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR PLICATION NUMBER: US 60/218,006
PRIOR FLING DATE: 2000-07-12
PRIOR FLING DATE: 2000-04-20
PRIOR FLING DATE: 2000-04-20
PRIOR PILING DATE: 2000-03-29
PRIOR PRIOR APPLICATION NUMBER: US 60/183,483
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-02-24
PRIOR PILING DATE: 1999-10-24
PRIOR PILING DATE: 1999-10-23
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PRIOR PILING DATE: 1999-10-8
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PRIOR FILING DATE: 1999-09-28
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US-10-027-632-70683
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Publication No. US20030204075A9
GENERAL INFORMATION
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Sing'
TITLE OF INVENTION: POlymorphisms in the Human Genome
FILE REPERSICE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
                  .2; DB 13;
4.9e-135;
                                                                                                                                                                                         2; Mismatches
                  Score 471.2;
                  18.4%;
99.6%;
Query Match
Best Local Similarity 99.6
Matches 470; Conservative
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PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-02-24
PRIOR PEDICATION NUMBER: US 60/165,218
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR PRICATION NUMBER: US 60/15,358
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-10-29
                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SOTTO 29374
LENGTH: 472
            FILING DATE: 2000-04-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 470; Conservative
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US-10-027-632-302414
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US-10-027-632-293974
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FITLE OF INVENTION: Polymorphisms in the Ruman Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION DATE: 2002-07-12
PRIOR PLING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
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PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR PILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR PILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-02-24
PRIOR PILING DATE: 2000-02-24
PRIOR PILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-18
PRIOR PILING DATE: 1999-09-18
PRIOR PILING DATE: 1999-09-18
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ORGANISM: Human
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LENGTH: 472
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GENERAL INFORMATION:
GENERAL INFORMATION:
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GENERAL INFORMATION:
GENERAL INFORMATION:
FIGURE OF INVENTION: Identification and Mapping of Single Nucleotide
ITILE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE:
GURERAL PERIONAL:
FILE SEPERATION:
FILE SEPERATION:
FILE OF INVENTION:

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18.4%; Score 471.2; DB 14; Length 472; 99.6%; Pred. No. 4.9e-135; tive 2; Mismatches 0; Indels 0;
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Pred. No. 4.9e-135;
2; Mismatches 0; Indels 0;
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US-09-18-995-22234

i Sequence 22234

i Septence No. US20030073623A1

i GENERAL INFORMATION:

i APPLICANT: Hyseq, Inc.

i TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBT.

I TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES

i TITLE OF INVENTION: NOVEL NOVEL OF SEQUENCES

i CURRENT APPLICATION NUMBER: US/09/918,995

i CURRENT APPLICATION NUMBER: US/09/235,076

i PRIOR FILING DATE: 1999-01-20

i NUMBER OF SEQ ID NOS: 38054

i SOFTWARE: FastSEQ for Windows Version 3.0

i ENGRALL SECTION NOVEL SEQUENCES

i TENGRALL SECTION NOVEL SEQUENCES

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PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-09
PRIOR FILING DATE: 1999-09
PRIOR FILING DATE: 1999-00
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 99.6%;
Matches 470; Conservative
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ORGANISM: Homo sapiens
FEATURE:
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; ORGANISM: Human
US-10-027-632-302414
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Patent No. US20020064855A1
Patent No. US20020064855A1
Patent No. US2002006485A1
APPLICANT: Inemischka, Ihor
APPLICANT: Lemischka, Ihor
APPLICANT: Moore, Kateri
TITLE OF INVENTION: GERISS THAT REGULATE HEMATOPIETIC BLOOD FORMING STEM
TITLE OF INVENTION: GERISS THAT REGULATE HEMATOPIETIC BLOOD FORMING STEM
TITLE OF INVENTION: GERISS THAT REGULATE HEMATOPIETIC BLOOD FORMING STEM
TITLE OF INVENTION: GERISS AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/789,919
CURRENT FILING DATE: 2001-02-21
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PatentIn Ver. 2.0
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                                                                                                Length 492;
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                                                                                           Query Match
17.1%; Score 438; DB 11; L
Best Local Similarity 100.0%; Pred. No. 9.6e-125;
Matches 438; Conservative 0; Mismatches 0;
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16.2%; Score 413.8; DB 9;
Best Local Similarity 60.2%; Pred. No. 7.4e-117;
Matches 735; Conservative 0; Mismatches 462;
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; LOCATION: (1)...(492)
; OTHER INFORMATION: n = A,T,C or
US-09-918-995-22234
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                                                 870 caddinarardccirrrigadararddaddarrigaaardarchrcrcrcgadirici
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bcudayaa
Mus musculus, Similar to hypothetical protein MGC31247, clone
IMAGE:5225131, mRNA.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 3441)
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Submitted (05-FEB-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA

NIH-MGC Project URL: http://mgc.nci.nih.gov

Contact: MgC help desk

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Jeffrey Green M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (house mouse)
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AUTHORS
TITLE
JOURNAL
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GenCore version
Copyright (c) 1993 - 2004
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Maximum Match 100%
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ALIGNMENTS

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BC023933 AK029115 AK036510 BX446508

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                                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 56 Row: o Column: 1
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis
This clone has the following problem: frame shifted.
Location/Qualifiers
                   Web site: http://www.nisc.nih.gov/
Contact: nisc_mgcahfgri.nih.gov
Contact: nisc_mgcahfgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Ghan,X., Gupta,J., Haghighi,P.,
Mansen,N., Ho,S.-L., Karlins,B., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
MCDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/mol_type="mRNA"
strain="FYB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5225131"
/tissue_type="Mammary tumor. C3(1)-Tag model. Infiltrating ductal_carcinoma. 5 month old virgin mouse."
/clone_lib="NAI CGAP_Mam6"
/lab_hōst="DH10B"
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Pred. No. 6e-273;
0; Mismatches 204; Indels
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922 c 970 g 732 t
Maryland
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Best Local Similarity 86.5%;
Matches 1353; Conservative
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Submitted (16-70L-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIERN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanaqawa 230-0045, Japan (E-mail:genome-resegsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-922, Cax:81-45-503-9216)
CDNA library was prepared and sequenced in Mouse Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to
                  Fukuda, S., Furumo, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishi, Y., Itoh, M., Kagawa, T., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Konda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nashi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, M., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Taqami, M., Taqawa, A., Takahashi, F., Takku-Akahira, S., Muranatsu, M., and Hayashizaki, Y., Yasunishi, A., Direct Submission
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/strain="C57BL/6J"
/db_xref="FANTOM_DB:4732493N06"
/db_xref="taxon:10090"
/clone="4732493N06"
/tissue_type="skin"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_sfage="10 days neonate"
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86.4%; Pred. No. 3.4e-272;
iive 0; Mismatches 206; Indels 7; (
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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db_xref="GI:26325102"
Adachi, J., Aizawa, K., Akimura, T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, B., Watahiki, M., Yoneda, Y., Inihikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. Sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to Prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full.length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3422)
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Nature 409 (6821), 685-690 (2001)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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                                                                                                                                              Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itch,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Arawawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Saito,T., Saito,T., Saito,T., Saito,T., Saito,T., Saito,T., Racota,K., Matsuda,H., Ashburner,M., Batalov,S., Casvant,T., Kacota,K., Matsuda,H., Ashburner,M., Batalov,S., Casvant,T., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Rigole,G., Tomita,M., Wagner,I., Washio,T., Sakai,K., Okido,T., Fuzuki,R., Tomita,M., Baldarelli,R., Barsh,G., Bakai,K., Okido,T., Furuo,M., Anno,H., Baldarelli,R., Barsh,G., Bakai,K., Okido,T., Furuo,M., Anno,H., Pictcher,C., Pulta,M., Garibold,M., Gustinoich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasak,H., Sato,K., Schonbad,M., Mazzarelli,J., Monbaerts,P., Nordone,P., Sato,K., Schonbad,M., Modriguez,I., Sakamoto,N., Sasak,H., Sato,K., Schonbad,M., Woltzeker,C., Wilming,L., Whishay,Y., Wang,K.H., Weltz,C., Whittaker,C., Wilming,L., and Hayashizaki,Y. Kawaji,H., Kohtsuki,S. Functional annotation of a full-length mouse cDNA collection and manyarana and Hayashizaki,Y. Rawaja,H., Nakana,H.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The FAWTOM Consortium and the RIKEN Genome Exploration Research Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNas

Nature 420, 563-573 (2002)

(1) Alzawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Eukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayasawa, M., Hiramcho, K., Thiracka, T., Hirozane, T., Hayashida, K., Hayasawa, T., Kojima, Y., Inch, M., Kagawa, T., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Inch, M., Kagawa, T., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kawai, J., Kojima, Y., Sakai, K., Ohno, M., Ohasto, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, K., Saitoh, H., Sakai, K., Saitoh, M., Saski, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Takaku-Akahira, S., Muramatsu, M., and Hayashizaki, Y., Takahashi, R., Takahashi, R., Tahaka, T., Tomaru, A., Toya, T., Yasunishi, A., Direct Submission

N. Submitted (16-UUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research Group, RIKEN Genomic Sciences Center (GSC), Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, Thiraki, The Littitute, Yokohama, Thirathitty://genome-gsc.riken.go.jp, Thiraki, Thirathitty://genome-gsc.riken.go.jp, Thiraki, Thirathitty://genome-gsc.riken.go.jp, Thirathitty://genome-gsc.riken.go.jp, Thirathitty://genome-gsc.riken.go.jp, Thirathitty://genome-gsc.riken.go.jp, Thirathitty://genome-gsc.riken.go.jp, Thirathitty://genome-gsc.riken.go.jp, Thirathitty://genome-gsc.riken.go.jp, Thirathitty://genome-gsc.riken.go.jp, Thirathitty://genome-gsc.riken.go.jp, Thirathitty://genome-gsc.riken.go.jp, Thirathitty://genome-gsc.riken.go.jp, Thirathitty://genome-gsc.riken.go.jp, Thirathitty://genome-gsc.riken.go.jp, Thirathitty://genome-gsc.riken.go.jp, Thirathitty://genome-gsc.riken.go.jp, Thirathitty://genome-gsc.riken.go.jp, Thirathitty://genome-gsc.riken.go.jp, Thirathitty://genome-gsc.riken.go.jp, Thirathitty://genome-gsc.riken.go.jp, Thirathitty://genome-gsc
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prepare mouse tissues.

Please visit our web site for further details.
URL:http://genome.gec.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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(db_xref="taxon:10090"
        Genome Res. 10 (11), 1757-1771 (2000)
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TGQLADGTPTGGDALVLGPWGKFLKDHSYKAAPVGCFRHVPLYDOWEDVKGHKVEV
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SKLIVPPRRIATAYOTGGRELLYEDGDSDDFWCHWSPLLHPVGWSRLEVVDK
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TOVGSTRTWAVDTVIGGERLLYEDGSDBPWCHWSPLLHPVGWSRLEVVDK
TOVGSTRTWASTAMRANGSTRUKSHWSSHALIPPATFCGCNDIELTPPKGYSTTOPF
AWRTYLEKTKSKAAPALINDCPNHGFKVGWKLEAVDLMSPRLICVATVKRVVHRIL
SIHPDGWDNSYDQWNDCSSPDIYPVGWCELIGYQLOPPSASPDTTPCKGKKKK
QFGTKKKK
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/note="unnamed protein product, H-L(3)MBT-LIKE PROTEIN (HYPOTHETICAL 79.1 KDA PROTEIN) homolog [Homo sapiens] (SPTR|Q969R5, evidence: FASTY, 90.9%ID, 100%length, arch=2109)
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RESULT 4 BX446508 LOCUS

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                                                                                                                                                                                                                                                                                    Craniata, Vertebrata, Buteleostomi,
Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 ;
                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Verte
Mammalia; Eutheria; Primates; Catarrhini; Hor
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
                                                                                                                       BX446508.1 GI:31031730
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96.9%;
                                                                                                                                                                                                   Homo sapiens (human)
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Matches 1034, Conservative
                                                                                                                                                                                                                                              Homo sapiens
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Best Local Similarity
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/organism="Homo sapiens"

/mol_type="maxA"

/db_Arzef="taxon:9606"

/dl_Clone="CSOD1070YF10"

/tlssue_type="PLACENTA COT 25-NORWALIZED"

/tlssue_type="PLACENTA COT 25-NORWALIZED"

/clone="lst strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and BcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

51 a 270 c 300 g 218 t 26 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAAGTCCAGAGCTGCCTGTCCGTCGAGAACATCAAGCAGGAAACAGAAACAGACTGAGCCT 1527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCAGGATGTGGATTTTGGCGACCTGTGGGTGGCCTTGAGCTGCTTTCTGTGTTTGTGAG 2187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           941 CATGCCTCCACCTGACTTTGGCTTKGAGACTGATCCTCTCTGTGTAAATTCTGCCCGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1057 CAAGTTCAAKACMRAGYGCTTTYCCBKCGARACWTCAAGCRGAAACAGACGA--TGAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      999 TCCTGCCTCCAGCCTGKCTTCTAGCT-GAAGCCAGCCCAGCG-TTYTTTACCACCACCAC
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Full-length cDNA libraries and normalization
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Livitrogen. This sequence belongs to sequence cluster 10409.f For
more information about this cluster, see
thtp://www.genoscope.ons.fr/
cip-bin/cluster.cgi?seq=CSODIO7ODCOSNPi&cluster=10409.f. Contact
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Mammalia; Eutheria; Primates; Cararhini; Hominidae; Homo.

E. (Bases I to 1201).

I. (Bases I to 1201).

I. (W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished

On Feb 15, 2001 this sequence version replaced gi:12906251.

Confact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 ENRY codex - France

BR 191 91006 ENRY codex - France

BR 191 91006 ENRY codex - France

BR 191 91006 ENRY codex - France

Email: seqref@genoscope.ons.fr www.genoscope.ons.fr

Invitrogen. This sequence belongs to sequence cluster 10409.f For http://www.genoscope.ons.fr/

Cgi-bhin/cluster.cgi?seq=CSDGG02BC07QPl&cluster=10409.f. Contact : Feng Liang Email: filiang@lifetech.com URL:

Feng Liang Email: filiang@lifetech.com URL:

Location/Qualifiers

Location/Qualifiers
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                                                AGATTCCTTTGTAGTTAAAGGGTCCAGTTCTGACTGGAGCCTCTAGAGAGCTGGGCTTGT
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AGENCOURT_7569887 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6074697
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Thissue Produrement: DcTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLCM2290 row: n column: 10
High quality sequence stop: 678.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Tissue Procurement: Low Stauch
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.G.E. Consorrium/LLNL at:
http://mage.lln.gov
Plate: LLCM1910 row: g column: 23
High quality sequence start: 13
High quality sequence start: 13
1 (bases 1 to 1080)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
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laboratory of Gerald M. Rubin (University of California Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."
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Best Local Similarity 98.2%; Pred. No. 1.6e-176;
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1744 1804 1864 1924 2044 1984 240 120 180 300 360 420 9 1625 CTCTGTGTAAATTCTGCCCGGTGCTGAAGGCTGGACGGTGGAGGACCTGCTGGGGCTCT 61 ccraegaccceccretrecrecereceresanagarenararandaceaece 121 TGAGGCCCCAGAACTCGTCTGTGAACCACCTTTTCCAGCCCAGAGTTCCCAAAGCTGGAAC 1 crcrororadaricreccosorecreredadecreadescedadeacerecaderesades GCTAGCTGCTCTTCCTTAAGATGGCCTCCCCCGACCCGCCACGGCCTCAGTTGC ACCAGTCATGTAAATTAAGTTCTAGAGCTCTCTGAGCAGGAGAAAAGGTCCCCTGACA 1685 CCTGGGACCCGCCTGTTGCTTCTGCCCTCCCTGTGGAAAGGTCTATATGACGGCCGCC AACGAGTCATGTAAATTAAGTTCTAGAGCAGCTCTCTGAGCAGGATAAGGTCCCCTGACA GTGAGTTGTGGGGGGGGGGCCTCTGCCTCAAAATTCACCAAGCAGAATGCCTCTCA Gaps 181 GCTAGCTGCCTGCTTCCTTAAGATGGCCTCCCCCCGGACCCGCCACGGCCCTCAGTTGC 4, Length 927; Indels Query Match 30.6%; Score 783; DB 13; Best Local Similarity 96.9%; Pred. No. 8.6e-174; Matches 809; Conservative 0; Mismatches 22; 1925 1985 301 à g ò

BQ927459
AGENCOURT 8822242 NIH MGC\_40 Homo sapiens cDNA clone IMAGE:6381422 5', mRNA Sequence.

RESULT 9 BQ927459 LOCUS DEFINITION

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AGENCOURT 7592644 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6050456
5', mRNA Sequence.
BQ217463.1 GI:20398863
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 membrane and secreted proteins
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                                                                                       Length 893;
                                    2 others
                                                                                                                          21; Indels
                                                                                     Score 773; DB 14;
Pred. No. 2e-171;
0; Mismatches 21;
                                    198 t
cancer genes encoding
Manuscript submitted."
                                                                                   Query Match
Best Local Similarity 96.8%;
Matches 811; Conservative
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AGENCOURT 10735964 MAPCL Homo sapiens cDNA clone IMAGE:6722445 5',
CA454956
CA454956.1 GI:24905191
             2104
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/organism="Homo sapiens"
/ord_type="makka"
/db_xref="taxon:6606"
/clone="IMAGB:6722445"
/cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231, hTERT-HME1
                                              480
                                                                                                                                                                                                                                                    601 AGGACATTGGGAGGAAGATGGCCTGAGTGTGCACTTTGGCTCTGCTACCTGCTCCTGAAG 660
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/note="Vector: pcMV-SPORT6; Site_1: EcoRV; Site_2: Not I;
/note="Vector: pcMV-SPORT6; Site_1: EcoRV; Site_2: Not I;
Subtracted with brain, liver, lung, kidney and muscle.
Directionally cloned. Priming method: oligo-dr. Average
insert size: 1800 bp. Library amplification: 26,000 fold.
Kristi A. Egland, James J. Vincent, Robert Strausberg,
Bungkook Lee & Ira Pastan: Discovery of new breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (1885) 1 to 893)
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contract: Robert Strausberg, Ph.D.

Email: Gapbs-remail.nih.gov
Tissue Procurement: Kristi A. Egland, Ira Pastan
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMA4285 row: c column: 21
High quality sequence stop: 691.
                                                                                                                                                                        541 GAGCTGCTTTCTGTGTTTGTGAGACTGACTCCCATTTCCTAAAGGAAATGCCCCGGGG
                         GCTCATGTTGTTTGGTCTCTGCTCCTAGCTCCCAGGATGTTGGGGAACCCAGCTTG
                                                                                                        481 TCTCGGCAGCTAAGAAGCAGTGACCAGGATGTGGTTTTTGCCGACCTGTGTGGTGGCCTT
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Homo sapiens
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KEYWORDS
SOURCE
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DEFINITION

ACCESSION

RESULT 10 CA454956

AUTHORS TITLE JOURNAL COMMENT

FEATURES

REFERENCE

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851 bp mRNA linear EST 20-JUN-2001 G2857991F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:4999294 5', B1092956. G1:14511286
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/mol_type="mRNA"

/mol_type="mRNA"

/db xref="taxon:9666"

/db xref="499294"

/cell_line="MGC36"

/cell_line="MGC36"

/cell_line="MGC36"

/cell_line="MGC36"

/coll_line="MGC36"

/coll_line="MGC36"

/lab host="DH10B"

/clone="Ib="NIH_MG"

/note="Organ: cervix, Vector: pCMV-SPORT6; Site_1: NotI; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.5 kb. Library prepared by Life
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NIH-MGC http://mgc.nci.nih.gov/.
                                                                           1035 GCCGIGGACCTGATGGAGCCCCGGCTCATCTGTGGGCCACGGTGAAACGAGTGGTGCAT
                                                                                                                   541 GCCGTGGACCTGATGGAGCCCCGGCTCATCTGTGTGGCCCACGGTGAAACGAGTGGTGCAT
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cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.row: e column: 23
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29.0%; Score 739.8; DB 12;
Best Local Similarity 97.5%; Pred. No. 1.3e-163;
Matches 836; Conservative 0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Location/Qualifiers
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                                                                                                                                                                                        Contract: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
    Tissue Procurement: ATCC/CTC/DTP
    CDNA Library Preparation: Life Technologies, Inc.
    CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
    DNA Sequencing by: Agencourt Bioscience Corporation
    Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
    http://ange.lln.gov
    Plate: LLAM1302 row: column: 09
    High quality sequence stop: 547.
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/lab_host="DHIOB (phage-resistant)"
/clone_lib="NJH MGC 72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2 kb. Library constructed by Life
Technologies."
2 246 c 253 g 164 t 2 others
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11H-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished
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                                                                                  Contact: Robert Strausberg, Ph.D.

Email: cgapbs.r@mail.nih.gov

Tissue Procurement: ATC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCM1303 row: d column: 07

High quality sequence stop: 763.

Location/Qualifiers
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National Institutes of Health, Mammalian Gene Collection (MGC)
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ilarity 93.4%; Pred. No. 4.5e-163;
Conservative 0; Mismatches 50;
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1055

09

120

9

Gaps

13;

Indels

43; 2.8e-162;

Pred. No. 2.Be ); Mismatches

1115

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996 TGCCCAAACCATGGCTTCAAGGTGGGCATGAAGCTGGAGGCCGTGGACCTGATGGAGCCC
                                                                                                                                                                                                                                        GAGAACTACTTGGAGAAGACCAAGTCGAAAGCCGCTCCATCGAGACTCTTTAACATGGAT
                                                                                                      1 GAGAACTACTIGGAGAGACCAAGTCGAAAGCCGCTCCATCGAGACTCTTTAACATGGAT
                                                                                                                                                                             61 recocharcearegerreaggregecargaagcregaegecegregaecergaregaegec
                                                                                                                                                                                                                                                                                         1116 GACGGCTGGGACAGCGAGTACGACCAGTGGGACTGCGAGTCCCCCAGACATCTACCCC
                                                                                                                                                                                                                                                                                                                             181 GACGGCTGGGACAGCGAGTACGACCAGTGGGACTGCGAGTCCCCAGACATCTACCCC
                                                                                                                                                                                                                  1056 CGGCTCATCTGTGTGGCCACGGTGAAACGAGTGGTGCATCGGCTCCTCAGCATCCACTTT
           11 Similarity 93.7%;
833; Conservative
                                                                  936
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/mol type="mRNA"
/mol type="mRNA"
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/lab host="Holl03" (T) phage-resistant)"
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Sfil (ggccgcctcggcc); Site 2: Sfil (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' and
3' adaptors were used in cloning as follows: 5' and
5' -ArrTAGAGGCCGAGAGCCCATATGGCC-3' and 3' adaptor sequence:
5' -ArrTAGAGGCCGAGAGCCCGACATGGTC-3' and 3' adaptor sequence:
5' -ArrTAGAGGCCGAGAGCCCGACATGGTC-3' and 3' adaptor sequence:
5' -ArrTAGAGGCCGAGAGGCCCGACATGGTC-3' (Ancre B = A,
C, or G and N = A, Cb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH MCC Library."
                                                                 1906
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                                                                                                                              1907 GIGAACTCTGTCTGCCTGAA-CGAGTCATGTAAA---TTAAGTTCTAGAGCAGCTCTCTG 1962
                                                                                                                                                                                                                                                                                       2082
600 GCCACGGCCCTCAGTTGCCAGGGATGGGGCCACCACTGTGTCACACTGTGGAATACAAGAAA 659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 914)
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: Gapbs-r@mail.nih.gov
Tisaue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:
http://image.lln.gov
Plate: LLCM1330 row: k column: 07
High quality sequence stop: 782.
                                                       GCCACGGCCCTCAGTTGCCAGGGATGGGGCCACCACTGTCACACTGTGGAATACAAGACA
                                                                                                                                                                                                                                      720 AGCAGGATAAGGTCCCCTGACAGTGAGTGTGTGTGGGGGGGAAGCTTCTGGCTCAAAAT
                                                                                                                                                                                                      AGCAGGATAAGGTCCCCTGACAGTGAGTTGTGTGGTGGGGGGCAGCCTCTGCCTCAAAAT
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ORGANISM
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AUTHORS
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855 bp mRNA linear EST 17-OCT-2001
60181058F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5245023 5',
mRNA sequence.
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                                       GTCGGCTGTGAGCTCACCGGCTACCAGCTCCAGCCTCCTGTGGCCGCAGAACCGGCC
                                                                                      361 AAAAGAATCCCGCCCACTAAGACGCGGACCCCTCAGACAGGGGTCCAAGAAGCCCCTGCTG
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                                                                                                                                        421 GAGGACGACCTCAGGGTGCCAGGAAGATCTCGTCGGAGCCTGTTCCTGGCGAGATCATT
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/mol type="mRNA"
/db_xref="txxxxn:9606"
/clone="InAGE:245023"
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/clone lib="MIH MGC_121"
/note="Organ: brain; Vector: pcWV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source anonymous pool of fetal brains, female age 20 weeks, female age 20 weeks, and male age 20 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3:5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note:
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                      Vertebrata; Buteleostomi;
                                                                                                                                    Email: gapbs.r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
http://inage.llnl.gov
Plate: LLAMIGIS row: d column: 16
High quality sequence start: 2
High quality sequence start: 2
Location/Qualifiers
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                                                                NIN-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butel.
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
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Pred. No. 4.3e-162;
0; Mismatches 16;
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this is a NIH MGC Library."
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AUTHORS
TITLE
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Search completed: February 4, 2004, 17:47:27 Job time : 5231 secs

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10-NOV-1999;
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Copyright (c) 1993 - 2004
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foetal liver
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AAS25416
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## ALIGNMENTS

Bandman O; C, Shah P;

Au-Young J, ;, Patterson

Yue H, Au Baughn MR,

Tang YT, Lu DAM,

Lal P, Yang J,

WPI; 2001-112727/12. P-PSDB; AAB60488. Azimzai 

Sequences AAF59590-AAF59643 represent cDNAs encoding 54 human cell cycle and proliferation proteins (CCYPR), AAB60453-AAB60506.

CCYPR and agonists of CCYPR are used to treat diseases or conditions associated with decreased expression of functional CCYPR, while CCYPR antagonists are used to treat diseases or conditions associated with overexpression of functional CCYPR, Monoclonal CCYPR, while CCYPR any be used in enzyme-linked immunosorbent associated with corpromise or corpromise. Corpromise or corpromise or corpromise or corpromise or corpromise or corpromise or corpromise or corpromise or corpromise. Corpromise or corpromise or corpromise or corpromise or corpromise or corpromise or corpromise or corpromise. Corpromise or corpromise or corpromise or corpromise or corpromise or corpromise or corpromise or corpromise or corpromise or corpromise or corpromi Human cell cycle and proliferation proteins and polynucleotides are used to treat, diagnose and prevent immune, developmental and cell signaling disorders and cell proliferative disorders including cancer Claim 5; Page 190-191; 205pp; English

Sequence 2555 BP; 577 A; 709 C; 722 G; 547 T; 0 other;

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AAI58732 standard; cDNA; 2781 BP.

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                       peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkineon's disease; hautingcin's disease; haremostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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Zhang J;
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Yang Y,
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     cytostatic;
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Wehrman T, Xu C, Xue AJ,
Goodrich R, Drmanac RT;
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 935; 10078pp; English.
nootropic; immunosuppressant;
                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0488725.
2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0653450.
2000US-0653450.
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Best Local Similarity 99.9%;
Matches 2552; Conservative
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Wang Z, F
Zhou P,
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                                                                                                                                                                                                                                              WO200153312-A1
                                                                                                                                        leukaemia; ss
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09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
                                                                                                                                                                                             Homo sapiens.
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Zhao QA,
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1201   ACCAGCTCCAGCCTCCTGTGGCCGCAGACCGCCACCGCTGAAGGCCAAAGGGCCA   1477   1426   ACCAGCTCCAGCCTCTGTGGCCGCAGACCCCCCCAAAGGGCCCAAAGGGCCCAAAGGGCCCAAAGGGCCCAAAGGGCCCAAAGGGCCCAAAGGGCCCAAAGGGCCCACTAAGGCCC   1477   1486   CACAGCTCAGCACCTCTGGCGCACTCTGGCGCCACTAGGCCC   1547   1486   CACAGCTCAGGACCCTCTGGCAGGAAAAGCCCTCTGCTGGAAAAAACACCCCCCACTAGGCCC   1547   1548   CACCCTCAGGACCCCTCTGCTGGAAAAAAACACCCTCAGGACCCCCCACTAGGCCC   1547   1548   CACCCTCAGGACCCCTCTGAGGACCCCCCACTAGGACCC   1549   1549   CACCCTCAGGACCCTCTGCTGGAAAAAACACCTCTGCTGGAAAAACACCTCTGCTGGAAAAACACCTCTGCTGGAAAAACACCTCTGCTGGAAACACCTCTGCTGGAAACACCTCTGCTGGAAACACCTCTGCTGGAAACACCTCTGCTGGAAACACCTTGCTGCTGCAGAACACCTTGCTGTGAAACACCTTGCTGTGAAACACCTTGCTGCTGCAGAACACCTTGCTGCTGCAGAACACCTTGCTGCTGCAGAACACCTTGCTGCTGCAGAACACCTTGCTGCTGCAGAACACCTTGCTGCTGCAGAACACCTTGCTGCTGCAGAACACCTTGCTGCTGCAGAACACCTTGCTGCTGCAGAACACTTGCTGCTGCAGAACACTTGCTGCTGCAGAACACTTGCTGCTGCAGAACACTTGCTGCTGCAGAACACTTGCTGCTGCAGAACACTTGCTGCTGCAGAACACTTGCTGCTGCAGAACACTTGCTGCTGCAGAACACTTGCTGCAGAACACTTGCTGCAGAACACTTGCTGCTGCAGAACACTTGCTGCTGCAGAACACTTGCTGCAGAACACTTGCTGCAGAACACTTGCTGCAGAACACTTGCTGCAGAACACTTGCTGCAGAACACTTGCTGCAGAACACTTACTT	2041 CTCAGCCTCATGTTGGTCCTCTGCTCCTAGCTCCCCAGGATGTTGGGGACCCCAG 2100 2268 CTCAGCCTCATGTTGGTCCTCTGCTCCTCAGCTCCCCAGGGATGTTGGGGACCCAG 2327 2101 CTTGTCTCGGCAGCTAAGAAGCAGTGACCAGGATGTTTGGCGACCTGTGTGGGGACCCAG 2327 2102 CTTGTCTCGGCAGCTAAGAAGCAGTGACCAGGATGTTGGAATTTTGGCGACCTGTGTGGTGG 2180 2328 CTTGTCTCGGCAGCTAAGAAGCAGTGACCAGGATGTGGATTTTGGCGACCTGTGTGGTGG 2387 2161 CCTTGAGCTTTTTTGTGAGACACTGCCCATTTCCTAAAGGAAATGCCCCC 2220 2388 CCTTGAGCTTTCTGTGTTTTGTGAGGACTGACTCCCATTTCCTAAAGGAAATGCCCCC 2447 2221 GGGGAGGACATTTGGGAGAGAAGGAACTGCACTTTCCTAAAGGAAATGCCCCC 2447 2221 GGGGAGGACATTTGGGAGAGAAAGGCCTGAGTGCACTTTGGCTCTGCTAACTGCTCCCT 2280 2448 GGGGAGGACATTGGGAGAAAGTGGCCTGAGTGCACTTTGGCTCTGCTACCTGCTCCT 2507
R 农 B 성 B 성 B 성 B 성 B 성 B 성 B 성 B 성 B 성 B	8 6 8 6 8 6 8 6
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                                                                                                                                                             The present invention relates to novel human secreted proteins (ABR47633-ABR48145) and their coding sequences (ACC50344-ACC50856). The proteins and their coding sequences are useful for the preparation of a diagnostic or pharmaceutical composition for diagnosing or treating a cardiovascular disorder (e.g., arrhythmia, tachycardia, cardiac arrest, coronary arteriosolerosis and myocardial ischaemia), neural disorders, immune system disorders, muscular disorders, reproductive disorders, gastrointestinal disorders and/or cancerous diseases and conditions, for wound healing and epithelial cell proliferation, to treat inflammation or infection, for treating thrombosis and arteriosclerosis, for treating thrombosis and arteriosclerosis, for treating thrombosis and arteriosclerosis, for treating entendosis and arteriosclerosis, for treating thrombosis and arteriosclerosis, for treating or preventing neural damage which occurs in neuronal disorders or neurodegenerative conditions such as Alzheimer's disease and Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                         Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic; vulnerary; antiinflammatory; nootropic; neuroprotective; antiparkinsonian; gene therapy; human; cardiovascular disorder;
                                                                              2568 TİGGAĞCCICIAGAĞAĞCIĞGĞCITĞIAİĞITCITITĞĞCCITTIĞİTCCIACLIAAATĞ
GAAGCCCCGCTAAAATAATTCATCCAAGATTCCTTTGTAGTTAAAGGGTCCAGTTCTGA
                 CTGGAGCCTCTAGAGCTGGGCTTGTATGTTCTTTTGGCCTTTTGTTCCTAAATG
                                                                                                         2401 AAGAAACCATGCCTGGAGGGCCGTGAACACAGAACCCTCAAGACAAGATGACAGAGCT
                                                                                                                                   2628 AAGAAACCAIGCCIGGAGGGCCCGIGAACACAGAACCCTCAAGACAAGGATGACGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human secreted proteins, useful for detecting, preventing, diagnosing, prognosticating, treating and/or ameliorating cardiovascular disorders such as arrhythmia
                                                                                                                                                                                                                                                                                                                                                                                               Human secreted protein coding sequence, SEQ ID 250.
                                                                                                                                                                                                                   2521 AATTAAACCCCCTGCTTGCTTGAGAAAAAAAA 2554
                                                                                                                                                                                                                                           2748 AATTAAACCCCTGCTTGCTTGAAAAAAAAA 2781
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                                                                                                                                                                                                                                                                                                                    CDNA; 3530
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19-JUL-2001; 2001US-306171P.
13-NOV-2001; 2001US-331287P.
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                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                 ACC50583 standard;
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disease, to enhance bone and periodontal regeneration and aid in tissue transplants or bone grafts, to prevent kin aging or hair loss, to stimulate growth and differentiation of haematopoietic cells and marrow cells when used in combination with other cytokines, to maintain organs before transplantation or for supporting cell culture of primary tissues, to increase or decrease differentiation or proliferation of embryonic stem cells, or to modulate mammalian characteristics or
                                                                                                                                                                                                                                                                                                                                                                                                                         TCAACAGTGATGCTGTGCTCCCCAGCCGGGTGTACTGGATCGCCTCTGTCATCCAGACAG
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                                                                                                                                                      Note: The sequence data for this patent was published in electronic format and is available from WIPO at
                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                        DB 25; Length 3530;
                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                           Sequence 3530 BP; 815 A; 945 C; 972 G; 790 T; 8 other;
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                                                                                                                                                                                                                                                                99.6%; Score 2544; Diarity 100.0%; Pred. No. 0; Conservative 0; Mismatches
                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                      Similarity
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ABZ71190-ABZ7147B represent cDNAs corresponding to 178 human secreted protein genes, and ABP00011-ABP00299 represent the proteins they encode. ABZ71479-ABZ71540 represent human secreted proteins they encode. ABZ71479-ABZ71540 represent human secreted proteins described by the secreted proteins and encompasses antibodies specific for the secreted proteins. The record of the secreted proteins in drug screening, and recombinant or vectors and host cells comprising a mucleic acid of the invention. The secreted proteins, and modulators of protein activity are useful for diagnosing, treating, ameliocating or preventing destrive disorders. Such conditions include disorders of the mouth, compasses and include cancers of these organs and tissues. The secreted proteins and their nucleic acids may also be used in the reatment of immune disorders, inflammation, infection, chromosome control seamless, and to promote wound healing. Nucleic acids of the invention may be used for chromosome identification, chromosome mapping, in gene therapy, for identifying individuals from minute markers. The present sequence represents a human secreted protein- and arkers. The present sequence represents a human secreted protein- and samples, and an arkers. The present sequence represents a human secreted protein-
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Best Local Similarity 100.0%; Pred. No. 0;
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Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antifinammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; gene; ss.
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The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB8040-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, reatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune (b) immune disorders e.g. Addison's disease, allergies, autoimmune (c) immune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as mycoardial ischamias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

Or printed specification, but was obtained in electronic format directly
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                                                                                         Novel 1405 isolated polypeptides, useful for diagnosis, treatment and prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders -
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                                                                                                                                                                                                                                             Claim 4; SEQ ID NO 419; 2081pp + Sequence Listing; English.
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Best Local Similarity 99.7'
Matches 2537; Conservative
WPI; 2002-122018/16.
P-PSDB; ABB89448.
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		ATCACCCACCTTCGGAAGATCTACTGGATGCGTTCCTTACCCCTCTTCAAGA ATCACCCCACCTTCCGGAAGATCTACTGTGATGCCGTTCCTTACCTCTTCAAGA ATCACCCCACCTTCCGGAAGATCTACTGTGATGCCGTTCCTTACCTCTTTCAAGA ATCACCCCACTTCCGGAAGATCTACTGTTTTGAGAAGGGATGAAGCTGGAGGCCG  [	TGATGATCTGTGGGGGGGCCCTCCACAGATGGCTTGGACTGGTTCTGCTACCATG TGATGATCTGTGGGGGGCCCTCCACAGATGGCTTGGACTGGTTCTGCTACCATG TGATGATCTGTGGGGGGGGCCCTCCACAGATGGCTTGGACTGGTTCTGCTACCATG TGATGATCTGTGGGGGGGGGCCCTCTGTCAGATGACTTGTTTTTTTT	CGAAAGCCGCTCCALCGAGACTTTCAACTGGGAGAACTAGGAGAAGAGAGAGAT 103 CGAAAGCCGCTCCALCGAGACTCTTTAACATGGATTGCCCAAACCATGGCTTCAAGGTGG 102 CGAAAGCCGGTCCATCGAGACTCTTTAACATGCCCAAACCATGGCTTCAAGGTGG 103 GCATGAAGCTGGAGGCCTGATGAGAGTCCCCAACCATGGCTTCAAGGTGG 109 GCATGAAGCTGGAGGCCTGATGAGAGCCCCGGCTCATCTGTGGCCCACGGTGG 108 GCATGAAGCTGGAGGCCTGATGGAGCCCCGGCTCATCTGTGGCCCACGGTGG 108 GCATGAAGCTGCAGCACCTGATGGAGCCCCGGCTCATCTGTGTGGCCCACGGTGA 108 AACGAGTGGTGCATCGGCTCCTCAAGGATCCACTTGATGGACCCACGGTGA 108 AACGAGTGGTGCATCGGCTCCTCAAGCATCCACTTTGACGGACAGGAGTACGACC 114	AGIGGGIGGACICCCCCAGACTTIGACGGCTGGGACGCAGACICGAGAGAGAGAGAGAGAGCGAGAGAGAG

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                    drug screening,
leukaemias and
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                                                                                                                                                 DB 22; Length 2380;
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and thrombolytic activity, cancer diagnosis and therapy, cassays for receptor activity, arthritis and inflammation, C.N.S disorders.

Note: The sequence data for this activity.
                                                      Note: The sequence data for this patent did not form part specification.
                                                                                                                                                                              3; Indels
                                                                                                                T; 0 other;
                                                                                                                                             Score 2374.2;
Pred. No. 0;
0; Mismatches
                                                                                                                  Seguence 2380 BP; 510 A; 664 C; 670 G; 536
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Best Local Similarity 99.9%;
Matches 2376; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                              nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
                                                                    GAAGAAACCATGCCTGGAGGGGCCGTGAACACAGAACCCTCAAGACAAGGATGACAGAGG
                                                                                                                      GAAGAAACCATGCCTGGAGGGGCCGTGAACACAGAACCCTCAAGACAAGGATGACAGAGC
                                                                                                    GTGTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                          peripheral nervous system; neuropathy; central nervous system; CNS; Alzhiener's; Parkinson's disease; hautingron's disease; haemostatic; amyotrophic lateral solerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l nucleic acids and polypeptides, useful for treating disorders as central nervous system injuries -
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Zhang J
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Yang Y,
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Wang Z, Wehrman T, Xh
Zhou P, Goodrich R,
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25-APR-2000; 2000US-0552317.
9-JUL-2000; 2000US-052317.
19-JUL-2000; 2000US-062312.
03-AJG-2000; 2000US-0653450.
14-SEP-2000; 2000US-0652191.
19-OCT-2000; 2000US-06533036.
29-NOV-2000; 2000US-059344.
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P-PSDB; AAM41362.
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Wang J, v
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Human transmembrane protein cDNA clone amy2\_li14.

Human, foetal brain, foetal kidney, melanoma, testis, amygdala, gene therapy, chromosome 22q13.31-13.33; ss.

fetal genetic Human cDNA sequences and clones derived from human fetal brain, kidney, melanoma, testis and amygdala cDNA libraries, useful in screening and therapy -

arrays the media from The present invention describes assemblages and computer readable recomprising novel human CDNA sequences and clones derived from human comprising novel human CDNA sequences and clones derived from human foctal brain, foetal kidney, melanoma, testis and amygdala CDNA libraries. ABA93702 to ABA9376 represent human CDNA sequences from present invention which encode the proteins given in ABB05562 to ABB05729. The human conde the proteins given in ABB0562 to therapy. The clones may be used in a variety of applications, for example they may be used in profiling assays, for providing large of human genetic meterial for implementing large-scale screening strategies and for treating diseases via gene therapy procedures.

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                    TCCTCTCTGTGTAAATTCTGCCCGGTGCTGTGAAGGCTGGACGGTGGAGGACCTGCTGGG
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leukaemia; antileukaemic; immunomodulator; therapy;
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primitive HSCs (PHSCs) such as umbilical cord cells, bone marrow cells and foetal liver cells. The encoded proteins (see AAY9176-93) are growth factors, transcription factors, splicing factors, capping factors, transport proteins, translation factors or replication factors that modulate HSC activity, especially differentiation or replication. The invention provides a claimed method for identifying PHSC-specific nucleic acids involving: creating a PHSC cDNA library and a non-PHSC immune cell library; and subtracting the 2 libraries. Also claimed are methods: for generating a stem cell/progenitor cell-from PHSCs; for identifying the presence of a PHSC in a sample; for identifying the presence in a sample of a compound that modulates HSC activity; for using such a compound to treat an immune system condition, especially laukaemia; for introducing exogenous nucleic acid into a HSC; and for ex vivo expansion of HSCs. Also claimed is a PHSC specifically expressing 1 of the claimed nucleic acids, such as the present sequence.
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The present invention relates to methods and compositions for detecting an angiogenesis-associated transcript in a cell in a patient. The method involves contacting a biological sample from a patient. The method involves contacting a biological sample from the patient with a polymucleotide that selectively hybridises to a sequence at least 80% identical to any of the angiogenesis-associated human polymucleotide sequences given in the specification. These candiogenesis associated polymucleotide sequences comprise genes that exhibit changes in expression levels as a function of time in tissue undergoing angiogenesis. The method and the polymucleotide sequences of the invention are useful for diagnosing and treating angiogenesis associated diseases e.g. cancer. The polymucleotide sequences are also useful in the gene therapy of such disorders. The angiogenesis-associated proteins encoded by the polymucleotide capiences are useful as a vaccine for therapeutic and prophylactic immunisation, ABXO8813 represent angiogenesis-associated
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Best Local Similarity 60.2%;
Matches 721; Conservative
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                                                                            Page 274-275;
                             undergoing angiogenesis
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     AGTCGAAAGCCGCTCCATCGAGACTCTTTAACATGGATTGCCCAAACCATGGCTTCAAGG 1017
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angiogenesis-associated disease, cancer, cytostatic, gene therapy,
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19-ARK-2001; 2001US-285475P.
03-AUG-2001; 2001US-310025P.
13-NOV-2001; 2001US-350666P.
29-NOV-2001; 2001US-354244P.
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polypeptide encoded by a polymucleotide (III) having a cDNA sequence (S1) from the 10912 nucleotide sequences as given in ABL77023 to ABL87934, (III) encoding (II) having a sequence (S2), a T cell population of (II), or antigen presenting cells that express (II).

(I) has cytostatic activity. An oligonucleotide (IV) that hybridises to (S1) can be used for detecting ovarian cancer in a patient's bloidgical sample professional to a patient with (IV), detecting the amount of polymucleotide hybridising to (IV) and comparing the amount to patient where the amount of polymucleotide hybridising to (IV) is detected preferably by polymerase chain reaction (PRN). (I) comprising catered preferably by polymerase chain reaction (PRN). (I) comprising context of (III) and/or (III) is useful for stimulating and/or expanding T cells with (III) or (II). (III) is useful in design and preparation of the tumour polymetrial in the trimulating expression of the tumour polymetrial context in the unique replace of the tumour polymetrial profession of the tumour polymetrial context in the library e.g., a tumour cDNA library using well known
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stomach, lung, prostate, pancreas, carcinoma, antitumour, cancerous,
cytostatic, gene therapy, antineoplastic, Wilm's tumour, adenocarcinoma,
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence 476 BP; 116 A; 124 C; 117 G; 112 T; 7 other;
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Best Local Similarity 95.5%;
Matches 358; Conservative (
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WO200194629-A2.

present invention describes a composition (I) comprising: carriers immunostimulants; and a polypeptide (II) of a ovarian tumour

The

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The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in comprises a sequence (S) selected from 847 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set
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02-OCT-2000; 2000US-237173P.
02-OCT-2000; 2000US-237278P.
02-OCT-2000; 2000US-237278P.
02-OCT-2000; 2000US-237294P.
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27-SEP-2000; 2000US-235711P.
27-SEP-2000; 2000US-235720P.
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28-SEP-2000; 2000US-236111P.
29-SEP-2000; 2000US-236842P.
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25-SEP-2000; 2000US-234924P.
25-SEP-2000; 2000US-235077P.
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27-SEP-2000; 2000US-235863P.
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Weaver Z;
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Soppet DR,
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treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarchinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, aguamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polymorphic human genomic sequences and related allele-specific probes and primers, useful for genetic analysis, e.g. diagnosis and monitoring of disease
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                                                                                                                                                                                                  1001 AAACCATGGCTTCAAGGTGGGCATGAAGCTGGAGGCCGTGGACCTGATGGAGCCCCGGCT
                                                                                                                                                                                                                                                                 1061 CATCTGTGTGGCCACGGTGAAACGAGTGGTGCATCGGCTCCTCAGCATCCACTTTGACGG
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                                                                                                                                                                                                                                   1 AAACCATGGCTTCAAGGTGGGCATGAAGCTGGAGGCCGTGGACCTGATGGAGCCCCGGCT
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/standard_name= "single nucleotide polymorphism"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 281.4; DB 24; Length 418; Pred. No. 1.2e-67; 0; Mismatches 8; Indels 0;
                                                                                                   Sequence 418 BP; 103 A; 112 C; 124 G; 76 T; 3 other;
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                                                                                                                                   Query Match
Best Local Similarity 97.3%;
Matches 285; Conservative
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Variation
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              This invention describes novel human nucleic acid segments (I) containing polymorphic sites. The polymucleotides of (I) are used for, e.g. correlating disease polymorphisms (or disease succeptibility) or other phenotypic traits (e.g. baldness, obssity, fertility, strength, response to drugs etc.); diagnosing and monitoring e.g. cancer, inflammation, heart or central nervous system diseases; detecting susceptibility to microbial infection; treating or preventing such diseases; forensic analysis; gene therapy, paternity testing; mapping genomic loci associated with phenotypic traits (and subsequent cloning
                                                                                                                                                                                                of the genes responsible); and the production of transgenic organisms. Antibodies raised against (I) are useful as diagnostic and therapeutic tools and in drug screening. AAH85144 - AAH87644 represent the human DNA sequences containing biallelic polymorphic sites described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                             2180 TTTGTGAGGACTGACTCCC--ATTTCCTAAAGGAAATGCCCCCGGGGAGGACATTGGGAG
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Pred. No. 4.6e-65;
0; Mismatches 2;
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98.6%;
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Matches 285, Conserv
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Drosophila melanogaster genomic polynucleotide SEQ ID NO 34672
ABL27733 standard; DNA; 3486
                                                                                                          (first entry)
                                                                                                          26-MAR-2002
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developmental biology; cell signalling; insecticide; cal; gene; ds. 3 Myers PWD, 23-MAR-2000; 2000US-191637P. 11-JUL-2000; 2000US-0614150. 23-MAR-2001; 2001WO-US09231 ij Drosophila melanogaster. pharmaceutical; gene; Adams M, WPI; 2001-656860/75 CORP NY WO200171042-A2 JĊ, 27-SEP-2001 (PEKE ) PE Venter 

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                                                                                                                                                                                                                                                                            WIPO
                                                                                                                           capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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                                                                                                             relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                       (ABBS7737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                   Score 266.4; DB 23; Length 3486;
Pred. No. 5e-63;
0; Mismatches 501; Indels 41;
                                                                          Claim 1; SEQ ID NO 34672; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                 Sequence 3486 BP; 939 A; 901 C; 869 G; 777 T; 0 other;
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55.6%;
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capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA (ABBS7737-ABB72072)
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                                                                                                                       The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                          Length 4379;
                                                                                                                                                                                        Sequence 4379 BP; 1162 A; 1151 C; 1118 G; 948 T; 0 other;
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10.4%; Score 266.4; DB 23;
Best Local Similarity 55.6%; Pred. No. 5.5e-63;
Matches 678; Conservative 0; Mismatches 501;
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## AAT23623 standard; cDNA to mRNA; 290 RESULT 15

BP

05-SEP-1996 AAT23623

Human gene signature HUMGS05481.

Search completed: February 4, 2004, 13:46:59 Job time: 691 secs

signature; messenger RNA; mRNA; relative abundance; frequency; 1; cloning; mapping; non-biased library; diagnosis; detection; typing; abnormal cell function; ss. human; Gene

sapiens Ното W09514772-A1

01-JUN-1995

94WO-JP01916 11-NOV-1994; 93JP-0355504 12-NOV-1993;

(MATS/) MATSUBARA K. (OKUB/) OKUBO K.

WPI; 1995-206931/27

Okubo K;

Matsubara K,

Identifying gene signatures in 3'-directed human cDNA library - for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human tissues

Claim 1; Page 1414; 2245pp; Japanese

A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in AAT19001-126837 and which is able to hybridise to part of human genomic DNA, cDNA or man, a Claimed. The GS (Gene Signature) sequences were obtained from 3' directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 

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3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.
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                                                                                                                                                                 Length 2555
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             Incyte Genomics, Inc. (US)
Location/Qualifiers
1.2555
/ organism="Homo sapiens"
/ mol_type="genomic DNA"
/ Mol_type="taxon:9606"
/ note="incyte ID No: 1868749CB1"
                                                                                                                                                                                           0;
                                                                                                                                                               DB 6;
   WO 0107471-A 90 01-FEB-2001;
Senomics, Inc. (US)
                                                                                                                                                               Query Match

100.0%; Score 2555;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2555; Conservative 0; Mismatches
      Patent:
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INSDAYLPSRYYWIASVIQTAGYRYLLRYEGFENDASHDFWCNLGTVDVHPIGHCAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AJ305226.1 GI:13940238
alternative splicing; H-1(3)mbt-like gene; H-1(3)mbt-like protein.
Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSA305226 3194 bp mRNA linear PRI 18-JAN-201
Homo sapiens mRNA for H-1(3)mbt-like protein, alternative variant
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                           GACAGTGAGTTGTGTGGGGGGGGGCTCTGCCTCAAAAATTCACCAAGCAGAATGCCT
                                                                                                                                                                              CTTGTCTCGGCAGCTAAGAAGCAGTGACCAGGATGTGGATTTTTGGCGACCTGTGTGGTGG
                                                                                                                                                                                                                                                            CTGTGTTTGTGAGGACTGACTCCCATTTCCTAAAGGAAATGCCCCC
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Molecular characterization of h-l(3)mbt-like: a new member of human mbt family
PEBS Lett. 507 (1), 119-121 (2001)
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/organism="Homo sapiens"
/or_type="mRNA"
/db_xref="taxon:9606"
/chromosome="22"
/map="22q13.31-33"
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Contact: nisc_mg/conhgri.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Benjamin,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,B., Legaspi,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tlongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
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NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-römail.nih.gov
Tissue Procurement: ATCC
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SIGNATION TO STUBBING SUGIYAME, T.

Direct Submission

Submitted (24-0CT-2001) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
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NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan, DNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA illi insert sequencing:
Research Association for Biotechnology (RAB); cDNA ilbrary
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: RAB and
                                        AK056443 3188 bp mRNA linear PRI 01-AUG-2002 Homo sapiens cDNA FLJ31881 fis, clone NT2RP7002829, weakly similar to Scm-related gene containing four mbt domains.
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Submitted (25-JAN-2001) Wismar J., Johannes Gutenberg Universitaet,
Institut fuer Genetik, Becherweg 32, 55099 Mainz, GERMANY
Location/Qualifiers
                                                                                                                  3107 GGÁGGACACATCTAGCTGCCATTGCAÁCCTCACTGGGCTCCCCAGÁCTCTGTGTGTGTGAGA 3166
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                                                                  Wismar, J. Molecular characterization of h-l(3)mbt-like: a new member
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/organism="Homo sapiens"
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/evidence=not_experimental
/product="FLOTO0162 protein"
/product="FLOT00162 protein"
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/db_xxref="di:18676530"
/translation="GANEDITEARARQSVEPVSTVSSLSRYTLIATQVPLYDQWEDVMK
/translation="GANEDITEARARQSVEPVSTVSSLSRYTLIATQVPLYDQWEDVMK
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LEVUDRSQVSRTRWANTDFVTGGRALRLLYREDDSDDDDDFWCHWMSPEDHIHVPVGMSRRVGH
GIKMSERRSDMAHHPPTRKTYCDAVPYLFKKVRAVTRGGWPEDGMKLBAIDPLMCAN
ICVATVCKVLLDGYLMICVDGGPSTDGLDWFCYHASSHAIFPATFCQKNDIELTPPKG
YEAQPFRWBRYLEKTKSKAAPSRLFNNDCPNHGFRVGMKLBAVDLMEPRLICVATVGR
VUNHLLSIHFDGWDSEYDQWVDCESPDIYPVGMCELTGYQLQPPVAAGVGSRGPFKEL"
84 a 1606 c 1626 g 1359 L
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                                 note="Start codon is not identified."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
GAGGGGCCGTGAACACAGAACCCTCAAGACAAGGATGACAGAGGCTGGAGGAGACACATCTAG
                                                                                                                        TGTGTTTGTGAGGACTGACTCCCATTTCCTAAAGAAATGCCCCCGGGGAGGACATTGG
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                                                                                                                                                                                                                                     AGGAAGATGGCCTGTGCTGCTTTGGCTCTGCTACCTGCTCCTGAAGGCCCCGCTAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (21-JAN-2002) Takahiro Nagase, Kazusa DNA Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jikuya,H., Takano,J., Nomura,N., Kikuno,R., Nagase,T. and O
The nucleotide sequence of a long cDNA clone isolated from
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/dev_stage="adult"
/note="vector:pBluescriptII SK plus"
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protein.
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2 (bases 1 to 5875)
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organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="FLJ00162"
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 Best Local Similarity 79.8
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Direct Submission

Submitted (12-MAR-2002) MIPS, Am Klopferspitz 18a, D-82152

Bartinszied, GERMANY

Clone from S. Wienmann, Molecular Genome Analysis, German Cancer
Research Center: DKFZ); Email s.wiemann@dkfz-heidelberg de;

sequenced by MediGenomix (Martinszied/Germany) within the CDNA
sequencing consortium of the German Genome Project. This clone
(DKFZp/FIL141) is available at the RZPD in Berlin. Please contact
the RZPD: Resourcenzentrum, Heubnerweg 6, 14659
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://mips.gsf.de/proj/cDNA/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LNSDAVLPSRVYWIASVIQTAGYRVLLRYEGFENDASHDFWCNLGTVDVHPIGWCAIN
SKILVPPRTIHAKFTDWKGYLMKRLVGSRTLPVDFHIKMVESWKYPPRQGMRLEVVDK
SKOSKTRWAVDTVIGGRLRLLYEDGDSDDDFWCHMKPPLIHPVGWSRRVGHGIKMSE
RRSDWAHPPIFRKIYCDAVYLPKKYVAVTEGGWFEEGMKLEAIDPLNLGNICVATV
CKVLLLDGYLMICVDGOSTDCLDWFCYHASSRAIFPRFCQKNDIELPPRGYSRAQTF
NWENYLEKTKSKAAPSRLFNMDCPUHGFKVGMKLEAVDLMEPRLICVATVKRVVHRLL
                                                                                                                   HOMO SADIELS MRNA; CDNA DKFZp7611141 (from clone DKFZp7611141);
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue type="amygdala"
/clone lib="761 (synonym: hamy2). Vector pSport1; host
DH10B; sites NotI + SalI"
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Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
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mol_type="mRNN"
db_xref="taxon:9606"
/map="22q13.31-13.33"
/clone="DKFZp7611141"
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'S. .1908
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1681   GTCTCCTGGGACCCGCCTGTTGCCCTCCCTGTGGAAAGGTCTATATGACGGGC   1740   1741	AK097052  N Homo sapiens cDNA FLJ39733 fis, clone SMINT2016122.  AK097052.  AK097052.1 GI.21756694  Oligo capping; fis (full insert sequence).  Homo sapiens (human)  M Homo sapiens  Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;  Mammalia: Butharia: Drinates: Craniata; Homo injae: Homo		Construction: Neith Research in Institute (Army) (Supplement of the Construction) of the Construction of the Construction; and Biotechnology Center, National Institute of Technology Center, National Institute of Technology Center, Institute of Technology Center, Sandian Institute of Technology Center, National Institute of Technology Center, Manager and RAB.  Location/Qualifiers  1. 2432  / organism="Homo sapiens" / mol_type="mRNA" / db_xref="taxon:9606" / clone="smNNY2016122" / tissue="type="small intestine" / clone="smNNY2016122" / tissue="type="small intestine" / clone="lib="sMINT2" / note="lolning vector: pME185FL3" / note="unamed protein product" / codon start=1 / protein_id="BAC04936.1" / db_xref="Gli:21756695" / translation="MCGIVGTREAFFSKTKRFCSVSCSRSYSSNSKKASI
8 6 8 6 8 6 8 6 8	RESULT 9 AK097052 LOCUS DEFINITION ACCESSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL COMMENT	FEATURES SOURCE
1670   GCATGAAGCTGGAGCCTGGACCTGATGGAGCCCGGCTCATCTGTGTGGCCACGGTGA   1729	1225 1224 2030 CTGCTCCTGACTTCTCTGTCTCTCTTGCCTGCAGAGCTCCTTCTTCTTT 2089 1225	CCGGCCTCTCTCTTTCACAGGTTTGCCTGTGTTCTCCGCCCTCTCTTCTCTGTGTGGGGGG	1381   AGATCTCGTCGGAGCTCTTCCTGGCGAGATCATTGCTGTGCGTGTGAAGGAAG

	RESULT 10  BC030864  BC030864  BC030864  BC030864  BC030864  BC030864.1  BC008CBC03086.1  BC008CBC03	Willalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Glbbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Youngha.C., Shevchenko,Y., Sandchaz,A., Whiting,M., Madan,A., Youngha.C., Shevchenko,Y., Bonifard,G.G., Blakesley,M.M., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Dickson,M.C., Razywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Scheil, J.E., Jones,S.J. and Marra,M.A.  TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  REPERRNCE 1 bases 1 to 3395)  REPERRNCE 2 bases 1 to 3395)  AUTHORS  Little Submitted (03-UN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
PTEKRAKULHKAAMSAKIGAFLHSQGTGQLADGTPTGQDALVLGPDWGKPLKDHSYKAA PVSCFKHYPLYDQWEDVDKGMKVEVLNSPAVLBARGYLAKTGARRLLAFGE  BVSCFKHYPLYDQWEDVDKGMKVEVLNSPAVLBASVQTAGGRELLAFGEDSDDFW  CHANGSPLIHPVGMSRRVGHELYDDRSGVERTHMAVVDTGGRLELLIEBGSDDDFW  CHANGSPLIHPVGMSRRVGHERKSDMAHHPFRKTYCDAPVRYLRKKRAYTEG  GWFEBGARLEADDLNICANICYRTVCKVLLDGYLDGYLPKKTYCDAPVLFKKKRAYTEG  GWFEBGARLEADDLNICANICYRTVCKVLLDGYLDGYLFKKYRAYTEG  GWFEBGARLEADDLNICANICYRTVCKVLLDGYLDGYLFKKYRAYTEG  GWFEBGARLEADDLNICANICYRTVCKVLLDGYLDGYLFKKYRAYTEG  GWFEBGARLEADDLNICANICYRTVCKVLLDGYLDGYLFKKYRAYTEG  GWFEBGARLEADDLNICANICYRTVCKVLLDGYLDGYLFKKYRAYTEG  GWFEBGARLEADDLNICANICYRTVCKVLLDGYLDGYLFKKYRAYTEG  GWFEBGARLEADDLNICANICYRTVCKVLLDGYLDGYLFKKYRAYTEG  GWFEBGARCHICATTGARGAGAGATTGANDGRAPSERDINPOGRHGFKYGMK  LEADDLNICANICANICANICANICANICANICANICANICANICA	QY         181 GGTGCAACCTGGGAACAGTGGATGCCACCCCATTGGCTGCTGCTCAACAGCAAGA 240           Db         899 GGTGCAACCTGGGAACAGTGCACCCCCATTGGCTGGTGCCATCAACAGCAAGA 958           QY         241 TCCTAGTGCCCCCACGGACCATCCATGCTGGTGGTGCCATCCACGCAACAGCAAGAGAACACTCCATGA 1018           QY         301 AACGGCTGGTGGCCTCCAGGACCATCCCCTGGATTCACCGACTGGAAGGGTACCTCATGA 1018           QY         301 AACGGCTGGTGGTGGCTCCCAGGACTTCCCCTGGATTTCCACTCAAGATGGTGGAGACA 1078           QY         361 TGAAGTACCCCTTTAGGCAGGCTTCCCGTGGATTTCCACATCAAGATGGTGGAGACA 1078           QY         361 TGAAGTACCCCTTTAGGCAGGCATCCGGGATTTCCCATCAAGATGGTGGAGACA 1078           QY         361 TGAAGTACCCCTTTAGGCAGGCATCCGGGCTGGAATTTCCACATCAAGATGGTGGAGACA 1078           QY         361 TGAAGTACCCCTTTAGGCAGGCATGCGGCTGGAAGTGGTGGACAAGTCCCAGGTGTCAC           QY         361 TGAAGTACCCCTTTAGGCAGGCATGCGGCTGGAAGTGGTGGACAAGTCCCCAGGTGTCAC           QY         421 GCACTCGCATGGAGCAAGAGACAAGTGGTGGACAAGTGGTGGACAAGTTCCCCAGGTGTCACCCTCTACGGCTCTACGGCTCTCTACGGCTCTCTACGGCTCTACGGCTCTCTACGGCTCTCTACGGCTCTCTACGGCTCTCTACGGCTCTCTACGGCTCTCTACGGCTCTCTACGGCTCTCTACGGCTCTCTACGGCTCTACGGCTCTCTACGGCTCTCTACGGCTCTCTACGGCTCTCTACGGCTCTCTACGGCTCTCTACGG	0.00   0.00

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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford Human Genome
Center, Library Arrayed by Sequencing Group at the Stanford Human Genome
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R. M.
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TOVSETRIMAVOTVIGGELELIZEDGOSDDDFWCHMMSPLIHPVGWRERVGHGIKMSD
CKVLLDGYLMICVDGGESTDGSDWFCYHASSHAIFPATFCOKNDIELTPPKGYETQPF
AWETYLEKTKSKAAAPARLFWNOCPHGFKVGYKLEAVDLMEPRLIGVATVKRVYHRLL
SIHFDGWDNEYDQWVDCESPDIYPVGWCELTGYQLQPPVSAEPNTFQKGKDTTKKKKK
DRSPSPQLPLPIESIKGESKKPLLEDNLEALGVSEPVPDDIIAVCVKREHQDISSP
DRSPSPQLPLFUESTKGRENN
127 t
911 c
951 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGTGCAACCTGGGAACAGTGGGATGTCCACCCCATTGGCTGGTGTGCCATCAACAGCAAGA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LiNL at: http://image.llnl.gov Series: IRAK Plate: 43 Row: i Column: 12. This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
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/strain="RYB/N"
/db xref="Taxon:10090"
/clone="MGC:31247 IMAGE:4211489"
/tissue_type="Tiver, normal.5 month old male mouse."
/lab_host="DH105"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AACATGTACCCCTCTATGACCAGTGGGAAGACGTCATGAAGGGGGATGAAGGTGGAAGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCAACAGTGATGCTGTGCTCCCCAGCCGGGTGTACTGGATCGCCTCTGTCATCCAGACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              creseracceserecrecrecearareasecrireaaareaceceaercareacrici
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
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Pred. No. 1.7e-297;
0; Mismatches 204; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="synonym: MGC31247"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene="4732493N06Rik"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 86.5%;
Matches 1353; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .3395
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ORIGIN
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Compresent(10989' .11290)
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Compresent(10989' .11290)
Compresent(10989' .11290)
11441. 11790

11455. 11594
11455. 11594
11456. 11594
11446. 124698
190in(17446. 127677,20088. 20170,20515. 20749,21230. 21295, 22966. 23082,23565. 24698)
Coin(17446. 17677,20088. 20170,20515. 20749,21230. 21295, 2966. 23082,23565. 24698)
Coin(17446. 17677,20088. 20170,20515. 20749,21230. 21295, 2966. 23082,235623.3 (novel protein similar to drosophila transcriptional repressor)
Cornel match: ESTS: Em:H22704 Em:AA351643 Em:AI364341
Em:T99539 Em:AG6448 Em:AI5653 Em:AI160926 Em:AA719364
Em:AI561948 Em:AI59746 Em:AI56079 Em:AA719364
Em:AI561948 Em:AI59746 Em:AI56076 Em:AA719368
Em:AI56218 Em:AI59789 Em:AA356192 Em:AA719368
Em:AA280121 Em:N56014 Em:T58851"
Corldencenot experimental
Join(17446. 17677,20088. 20170,20515. 20749,21230. 21295, 22966. 23082,23565. 23367)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein id="CAB65071.1"

/db xref="GI.6572271"

/db xref="SPTREMBL:Q9UGS4"

/translation="MVESMKYPFRQGMRLEVVDKSQVSRTRMAVVDTVIGGRLRLLYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DGDSDDDFWCHMWSPLIHPVGWSRRVGHGIKMSGYBAQTFNWENYLEKTKSKAAPSRL
MNDCDNHGEKVGWKLARADDLMEPRLLCAPUYKNYNTRILLEI HBOGWDSESYDGWYDCB
SPDIYPVGWCELTGYQLQPPVAAEBATPLKAKEATKKKKQYGKKRRI PPTKTRPLR
QGSKKPLLEDDPQCARKISSBPVPGEIIAVRVKBEHLDVASPDKASSPELPVSVENIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(join(28566, .28769,29910, .30076,30602, .32311, 32869, .33046,34152, .34282))
//gene="dd756023.1"
complement(join(<28566, .28769,29910, .30076,30602, .32311, 32869, .33046,34152, .34282))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="match: cDNAs: Em:U08018
match: ESTs: Em:AA128077 Em:AA326017 Em:W58996 Em:A1460232
Em:AA367412 Em:AA126901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
/evidence=not_experimental
/product="dJ756G23.3 (novel protein similar to drosophila
transcriptional_repressor)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  match: proteins: Tr:055226 Sw:002833 Sw:P22792 Sw:Q01129 Tr:086637"
true left end of clone RP5-979N1 is at 89849 in this sequence. T
true right end of clone RP1-85F18 is at 80441 in this sequence.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="match: proteins: Tr:075996 Tr:Q24191 Wp:CE06250
                                                                                                                                                                                                                                                                                                                                                                                                   .296 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                       matches 1.
                                                                                                                                                                                                                                                                                                                             /clone lib="RPCI-4"
2172. _2466
/note="AluSg1 repeat: matches 1
complement(10832. .11352)
/note="match: GSS: Em:AQ266638"
complement(10989. .11290)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /noie="match: STS: Em:G14475"
complement(24350. .24620)
/note="match: STS: Em:G43605"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Em:G14931"
                                                                                                                                        /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (24311. .24697)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (24449. .24697
                                                                                                                                                                /mol_type="genomic_DNA"
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                                                                                                                                                                                                                                                                  /map="q13.31-13.33"
/clone="RP4-756G23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="match: STS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene="dJ756G23.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fr:076931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24698
                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct submission

Submitted (11-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requesters: clonerequestedsanger.ac.uk

On May 27, 1999 this sequence version replaced gi:4775627.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Ent. EMBL; Sw.; SWISSERCT; Tr.; TREMBL; Wp:, WORDEP: Information on the WORMPEP database can be found at the proper and according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as annotated repeats, but not necessarily within known annotated repeats, but not necessarily within known annotated repeats, but not necessarily within known annotated repeats sequence elements. Where the sequence is an annotation using the 'unsure' feature key. This sequence was generated from part of bacterial clone contigs of human chromosome 22, constructed by the Sanger Centre Chromosome 22, here in the manner in moration can be found at
                                  GACCCCTCAGACAGGGGTCCAAGAAGCCCCTGCTGGAGGACGACCCTCAGGGTGCCAGGA 1380
                                                                                              1931 GGCCCCTCAGACAGGCTCCAAGAAACCCTTACTGGAGGACAACCTTGAGGCTTTGGGG- 1989
                                                                                                                                                                    1440
                                                                                                                                                                                                                               1441 TAGACGTGGCCTCGCCCGACAAGGCTTCAAGTCCAGAGCTGCCTGTCTCCGTCGAGAACA 1500
                                                                                                                                                                                                                                                                                                                                                  2045 AGGACATTTCCTCGCCTGACAGTCGCCCAGTCCACAGCTGCCTCTTCCCATTGAGAGCA 2104
                                                                                                                                                                                                                                                                                                                                                                                                                           1501 TCAAGCAGGAAACAGACGACTGAGCCTT-CCTGCCTCCAGCCTGGCTTCTAGCTGGAAGC 1559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HS756G23 B9948 bp DNA linear PRI 12-JAN-2001 Human DNA sequence from clone RP4-756G23 on chromosome 22q13.31-13.33 Contains the 5' part of a gene similar to drosophila transcriptional repressor, the 3' end of the gene for a novel Leucine Rich Protein, the RANGAPI gene for Ran GTPase activating protein 1, ESTS, STS, GSSs and three putative CpG islands, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMPORTANT: This sequence is not the entire insert of clone 847-756033 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP4-756023 is at 1 in this sequence. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
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RP4-756G23 is from the library RPCI-4 constructed by the group
Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2105 TCAAGCAGGAGGAACAACTGAGACTTCCCTGGCATCAGCCTGGACCCTAACTGAAGCC
                                                                                                                                                             AL035681.13 GI:4902689
HTG; CpG island; Ran GTPase activating protein; RANGAP1.
Homo sapiens (human)
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Mammalia; Butheria; Primates;
1 (bases 1 to 89948)
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DEFINITION
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AUTHORS
TITLE
JOURNAL
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KEYWORDS
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COMMENT

SOURCE

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/protein_id="CAB63073.1"
| db_xref="G1:657273"
| db_xref="SW1557273"
| db_xref="SW1557575"
| translation="MASEDIAKLAETLAKTQVAGGQLSFKGKSLKLNTAEDAKDVIKE
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/product="dJ756G23.2 (Ran GTPase activating protein 1)
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                                                                                                                                                                                                                                                 DB 9;
                                                                                                                                                                                                                                        Score 1132.4; DB 9
Pred. No. 3.3e-279;
0; Mismatches 1;
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/codon_brail=1
/product="dJ756G23.1 (novel Leucine Rich Protein)"
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BLGHNPLTYAGEBEDGIALPGERELLLDGGALQALGFRAHCPRLHTLDLRGNQLDTL
PPLQCSPQQAREIRIRLQGNPLWCGCQARPLIEWIARARYRSDGACQSPRRIRGBALDALR
PPLCCFGDARQEBEELERRAVGGPRPRGPRGPRGPGERAVAPCPRACVCVPESRHS
SCEGCCIQAVPRGFPSDTQLLDLRRNHFPSVPRAAPFGLGHJVSLHLQHCGTAELEAG
ALAGICRLIYIYLSDNQLAGISAAALEGAPRIGYLYLERNRFLQVFGAALRALPSLFS
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VPTGALEGLPALLELQLSGNPLRALRDGAFQPVGRSLQHLFLNSSGLEQICPGAFSGL
GPGLQSLHLQKNQLRALPALPSLSQLELIDLSSNPFHCDCQLLPLHRWLTGLNLRVGA
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44433. 44535,46288. 46417,47734. 47420,49447. 49531,
49617. 49716.50137. 50250,51374. 51532,54872. 55006,
58090. 58269,61523. 61582,68026. 68153,74359. 74470))
Jenne-RANGARI"
//note="RANGARI"
//note="RANGARI"
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35563. .35664
hote="51 copies 2 mer ta 86% conserved"
36802. .36970
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/evidence=not_experimental
complement (32183. 32620)
/gene="d4756623.1"
/note="match: GSS: Em:AQ389159"
32627. 33079
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15161. .35287
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complement(39054. .39059)
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39047. .39317
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941 AGCGGTTGGTGGGTTCCAGGACACTTCCTGCAGACTTCCATATCAAGATGGTGGAAAGCA 1000
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                                                                                                                                                                                                                                                                                                                                                                     641 AACATGTACCCCTCTATGACCAGTGGGAAGACGTCATGAAGGGGGATGAAGGTGGAAGTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      481 ATGGTGACAGTGACGACGTCTGGTGCCACATGTGGAGCCCCCTGATCCACCCAGTGG
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44.2%; Score 1128.2; DB 10

Best Local Similarity 88.9%; Pred. No. 3.9e-278;

Matches 1220; Conservative 0; Mismatches 153;
                                                                                                                                    1: mbt repeat"
947 g 722 t
'note="Region: mbt repeat'
                   1267. .1545
/gene="M4mbt"
/note="Region: mbt rv
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/gene="M4mbt"
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                                                          24525 TTCTTTGGCCTTTTGTTCCTACCTAATGAAGAAACCATGCCTGGAGGGGCCGTGAACA 24584
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                      TTCTTTTGGCCTTTTGTTCCTACCTAAATGAAAACCATGCCTGGAGGGCCGTGAACA 2430
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Mus musculus M4MBT variant B (M4mbt) mRNA, complete cds;
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SIHPDGWDNEYDQWYDCESPDIYPVGWCELTGYQLQPPVSAEPNTPQKGKDTTKKKKK
QFGKKRKRIPSAKTRPLRQGSKKPLLEDNLEALGVSEPVPDDSRPVHSCLFPLRASSR
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TGQLADGTPTGQDALVLGFDWGKFLKDHSYKAAPVSCFKHVPLYDQWEDVWKGMKVEV
LNSDAVLPSRVYWIATVIQAAGYRVLLRYEGFENDASHDFWCNLGTVDVHPIGWCAIN
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RRCDMSHHPTFRKIYCDAVPYLFKKVRAVYTEGGWFEEGMKLBAIDPLNLGSICVATI
CKVLLDGYLMICVDGGPSTDGSDWFCYHASSHAIFPPATFCQKNDIELTPPKGYETQPF
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SSYLEESSEAENEDREAGELPTSPLHLFSSANNRSLDGSGSEPAVCEMCGIVGTREAF
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 3399)
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Markus, J., Felkova, S., Sramko, M., Wolff, L. and Bies, J.,
Direct Submission
Submitted (14-FEB-2003) Department of Molecular Virology, Cancer
Research Institute of Slovak Academy of Sciences, Vlarska 7,
Bratislava, Slovak Republic
Location/Qualifiers
                                                                                                              CAGAACCCTCAAGACAAGGATGACAGAGCTGGAGGACACATCTAGCTGCCATTGCAACCT
                                                                                                                                                                                                                              Markus, J., Feikova, S., Sramko, M., Wolff, L. and Bies, J. Cloning and molecular characterization of the novel murine M4mbt encoding a nuclear zinc finger protein with four mbt Unpublished
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product="M4MBT variant B"
protein_id="AAO84917.1"
db_xref="G1:29569826"
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/gene="M4mbt"
/note="Region: mbt repeat"
916 . 1212
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/strain="Swiss Webster"
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Markus,J., Feikova,S., Sramko,M., Wolff,L. and Bies,J.
Cloning and molecular characterization of the novel murine gene Mambt encoding a nuclear zinc finger protein with four mbt domains Unpublished
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              CGCCAAAAGGTTATGAGGCACAGACTTTCAACTGGGAGAACTACTTGGAGAAGACCAAGT
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Markus, J., Felkova,S., Sramko,M., Wolff,L. and Bies,J.
Direct Submission
Submitted (14-FEB-2003) Department of Molecular Virology,
Research Institute of Slovak Academy of Sciences, Vlarska
Bratislava, Slovak Republic
Location/Qualifiers
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'gene="M4mbt"
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LNSDAVLPSRYVWIATVIOJAAGYKVLLKYEGSPENDASHDFWCNLGFVDVHPIGWCAIN
SKLLVPPRTIHAKFTDWKSYLMKRLVGSRTLPADFHIKMVBSMKYPPRQGKELEVVDK
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Pred. No. 3.3e-211;
0; Mismatches 206;
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Genes that regulate hematopoietic blood forming stem cells and uses
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Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                    2352 AGAGAGCTGGGCTTGTATGTTCTTTTGGCCTTTTGTTC 2389
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Princeton University (US)
Location/Qualifiers
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